

(19)



Europäisches Patentamt
European Patent Office
Office européen des brevets

(11) Publication number:

**0 340 948
A1**

(12)

EUROPEAN PATENT APPLICATION

(21) Application number: 89304034.5

(22) Date of filing: 24.04.89

(51) Int. Cl. 4: **C12N 15/00 , C12P 21/02 ,
A01N 63/02 , C12N 1/20 ,
C07K 7/10 , //(C12N1/20,
C12R1:39)**

(30) Priority: 28.04.88 US 187167

(43) Date of publication of application:
08.11.89 Bulletin 89/45

(64) Designated Contracting States:
AT BE CH DE ES FR GB GR IT LI LU NL SE

(71) Applicant: **Mycogen Corporation**
5451 Oberlin Drive
San Diego, CA 92121(US)

(72) Inventor: **Wilcox, Edward**
2623 Mary Lane Place
Escondido CA 92025(US)
Inventor: **Edwards, David L.**
13824 Recuerdo Drive
Del Mar CA 92014(US)
Inventor: **Schwab, George E.**
316 Prospect Avenue
La Jolla CA 92037(US)
Inventor: **Thompson, Mark**
510 Stratford Court
Del Mar, CA 92014(US)
Inventor: **Culver, Paul**
644 Stratford Drive
Encinitas, CA 92024(US)

(74) Representative: **Perry, Robert Edward et al**
GILL JENNINGS & EVERY 53-64 Chancery
Lane
London WC2A 1HN(GB)

(54) Novel hybrid pesticidal toxins.

(57) The invention concerns novel hybrid pesticidal toxins. These toxins are expressed as the fusion protein of a chimeric gene. Specifically exemplified is a novel B.t. hybrid toxin. These novel toxins have increased toxicity against target pests. The invention also concerns a process for preparing a hybrid virus having an altered insect host range.

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NOVEL HYBRID PESTICIDAL TOXINS

Background of the Invention

Bacillus thuringiensis (B.t.) is widely used for the microbial control of insects. The active component has been identified as a proteinaceous paraspore also described as a crystal. Following ingestion by the insect host the crystal is processed by gut proteases to the active protease-resistant form which is toxic. Toxicity is postulated to follow binding of the active form of the toxin to the insect cells resulting in disruption of cellular integrity through a receptor mediated process (Knowles, B.H. et al. [1984] FEBS 168:197-202).

A comparison of amino acid sequence for the protease activated form of B. thuringiensis var. kurstaki HD-1 and HD-73 reveals that the amino-terminal (N-terminal) half of the protein is highly conserved whereas the carboxy-terminal (C-terminal) is highly substituted in sequence. In U.S. Patent 4,467,036 B. thuringiensis var. kurstaki HD-1 is disclosed as being available from the NRRL culture repository at Peoria, IL. Its accession number is NRRL B-3792. B. thuringiensis var. kurstaki HD-73 is also available from the NRRL under accession number NRRL B-4488.

In addition to HD-1 and HD-73, the presence of an N-terminal conserved or constant region and a C-terminal highly substituted or variable region in the active toxin has been demonstrated for B. thuringiensis var. berlineri and var. aizawa.

Schnepf, E.H. and Whitely, H.R. (1985) J. Biol. Chem. 260:6273-6290 have demonstrated that deletions of the amino and carboxy termini result in a loss of toxicity indicating that both regions of the active toxin are required for toxicity.

Brief Summary of the Invention

The subject invention concerns novel hybrid pesticidal toxins. Specifically exemplified is an insecticidal fusion protein expressed as a single polypeptide product of a hybrid gene comprising a cytotoxic agent and a specific insect gut cell recognition ("binding") protein to direct the cytotoxic agent to the host target. Details for the construction of a hybrid B.t. toxin are disclosed. The cytotoxic agent is an ADP-ribosylating enzyme. For example, the cytotoxic agent can be the A fragment of the diphtheria toxin, plus the B fragment of the diphtheria toxin which has been truncated at the carboxyl-terminus to remove the eukaryotic binding region. The diphtheria toxin gene 3' recognition domain is replaced with a synthetic DNA linker region to which a gene encoding the insect gut epithelial cell recognition portion of Bacillus thuringiensis var. kurstaki HD-73 is ligated.

The purpose of the synthetic DNA linker is to join pieces of otherwise non-ligating segments of DNA. In the subject invention, it is a critical element of the invention because it must be of a suitable length and amino acid composition to minimize susceptibility to insect protease cleavage. Thus, the peptide linker should be as short as possible, e.g., four or less amino acids, and it should not contain lysine residues. There are other considerations in the use of a suitable linker. For example, the linker should maintain the correct reading frame and it should maintain a continuum in the hydropathy profile of the primary structure of the protein.

The novel hybrid B.t. gene can be transformed into a suitable host to produce the toxin which can be recovered by standard biochemical procedures. Alternatively, the transformed host containing the novel hybrid B.t. gene can be used per se as an insecticide, as disclosed hereinafter. Though B.t.k. HD-73 is specifically exemplified herein, the invention includes other microbial insecticides.

Table 1 discloses the DNA encoding the half-length hybrid toxin.

Table 2 discloses the DNA encoding the quarter-length hybrid toxin.

Table 3 discloses the amino acid sequence of the half-length hybrid toxin.

Table 4 discloses the amino acid sequence of the quarter-length hybrid toxin.

Table 5 gives molecular weights of polypeptides present in S α NPV and H α NPV LOVAL preparations determined from relative electrophoretic mobilities.

Table 6 shows hybrid virus infectivity.

Table 7 gives relative molecular weights of polypeptides as determined by electrophoretic mobility.

The process, described herein, can be applied to the C-terminal variable portion of active B.

thuringiensis toxins other than var. kurstaki HD-73. These include those B.t.'s which possess a variable region in the C-terminal half of the active toxin. Examples of such B.t.'s are B.t. var. israelensis, active against mosquitoes; B.t. var. san diego and B.t. var. tenebrionis, active against coleoptera; and B. sphaericus, active against mosquito larvae. Cultures exemplifying the above are as follows:

- 5 Bacillus thuringiensis var. kurstaki HD-1--NRRL B-3792; disclosed in U.S. Patent 4,448,885
Bacillus thuringiensis var. israelensis--ATCC 35646
Bacillus thuringiensis var. san diego--NRRL B-15939

The following B. thuringiensis cultures are available from the United States Department of Agriculture (USDA) at Brownsville, Texas. Requests should be made to Joe Garcia, USDA, ARS, Cotton Insects
 10 Research Unit, P.O. Box 1033, Brownsville, Texas 78520 USA. B. thuringiensis HD2

- B. thuringiensis var. finitimus HD3
B. thuringiensis var. alesti HD4
B. thuringiensis var. kurstaki HD73
B. thuringiensis var. sotto HD770
 15 B. thuringiensis var. dendrolimus HD7
B. thuringiensis var. kenyae HD5
B. thuringiensis var. galleriae HD29
B. thuringiensis var. canadensis HD224
B. thuringiensis var. entomocidus HD9
 20 B. thuringiensis var. subtoxicus HD109
B. thuringiensis var. aizawai HD11
B. thuringiensis var. morrisoni HD12
B. thuringiensis var. ostrinae HD501
B. thuringiensis var. tolworthi HD537
 25 B. thuringiensis var. darmstadiensis HD146
B. thuringiensis var. toumanoffi HD201
B. thuringiensis var. kyushuensis HD541
B. thuringiensis var. thompsoni HD542
B. thuringiensis var. pakistani HD395
 30 B. thuringiensis var. israelensis HD567
B. thuringiensis var. indiana HD521
B. thuringiensis var. dakota
B. thuringiensis var. tohokuensis HD866
B. thuringiensis var. kumanotoensis HD867
 35 B. thuringiensis var. tochigiensis HD868
B. thuringiensis var. colmeri HD847
B. thuringiensis var. wuhanensis HD525

Other pesticidal toxins which can be used include those of entomopathogenic fungi, such as beauverin of Beauveria bassiana and destruxins of Metarrhizium spp.; or the broad spectrum insecticidal compounds,
 40 such as the avermectins of Streptomyces avermitilis. Cultures exemplifying the above are as follows:

- Bacillus cereus--ATCC 21281
Bacillus moritai--ATCC 21282
Bacillus popilliae--ATCC 14706
Bacillus lentimorbus--ATCC 14707
 45 Bacillus sphaericus--ATCC 33203
Beauveria bassiana--ATCC 9835
Metarrhizium anisopliae--ATCC 24398
Metarrhizium flavoviride--ATCC 32969
Streptomyces avermitilis--ATCC 31267

50 The technology of the invention is not limited to the use of diphtheria toxin as the cytotoxic agent as a variety of enzymes that inhibit protein synthesis can be used, for example, the ribosome inactivators such as ricin, dianthin, saporin, gelonin, tritin, abrin, and modeccin, as well as enzymes from barley seeds, rye seeds, wild beans, and corn seeds (see Stripe, F., and Barbieri, L., [1986] FEBS 195:1-8).

The subject invention is not limited to toxins active against insects, but also includes B. thuringiensis
 55 toxins active against animal parasitic nematodes, and plant parasitic nematodes. In general, any pesticide can be used. For example, it can be a polypeptide which has toxic activity toward a eukaryotic multicellular pest, such as insects, e.g., coleoptera, lepidoptera, diptera, hemiptera, dermaptera, and orthoptera; or arachnids; gastropods; or worms, such as nematodes and platyhelminths. Various susceptible insects

include beetles, moths, flies, grasshoppers, lice, and earwigs.

The subject invention also includes a process for altering the insect host range of a nuclear polyhedrosis virus (NPV) by re-associating solubilized envelope proteins from one occluded NPV to another to produce a hybrid virus having an altered NPV insect host range.

Table 1. DNA encoding half-length hybrid toxin

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      10      20      30      40      50      60      70      80
GTGAGCAGAAAACTGTTGCGTCAATCTTAATAGGGGCGCTACTGGGGATAGGGGCCCCACCTTCAGCCCATGCAGGCGC

      90     100     110     120     130     140     150     160
TGATGATGTTGTTGATTCCTTCTAAATCTTTGTGATGGAATACTTTCTTCGTACCACGGGACTAAACCTGTTATGTAG

      170     180     190     200     210     220     230     240
ATTCCATTCAAAAAGGTATACAAAAGCCAAATCTGGTACACAAAGAAATTATGACGATGATTGAAAAGGGTTTATAGT

      250     260     270     280     290     300     310     320
ACCGACAATAAATACGACGCTGCGGGATACTCTGTAGATAATGAAAACCCGCTCTCTGGAAAAGCTGGAGGCGTGGTGAA

      330     340     350     360     370     380     390     400
AGTGACGTATCCAGGACTGACGAAGGTTCTCGCACTAAAAGTGGATAATGCCGAAACTATTAAGAAAGAGTTAGGTTTAA

      410     420     430     440     450     460     470     480
GTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTTATCAAAAGGTTCCGGTGATGGTGCTTCGCGTGTAGTG

      490     500     510     520     530     540     550     560
CTCAGCCTTCCCTTCGCTGAGGGGAGTTCTAGCGTTGAATATATTAATAAAGTGGGAACAGGGCAAAGCGTTAAGCGTAGA

      570     580     590     600     610     620     630     640
ACTTGAGATTAATTTTGAACCCGTTGAAAACCGTGGCAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAA

      650     660     670     680     690     700     710     720
ATCGTGTGAGGCGATCAGTAGGTAGCTCATTGTATGCATAAATCTTGATTGGGATGTCATAAGGGATAAACTAAGACA

      730     740     750     760     770     780     790     800
AAGATAGAGTCTTTGAAAGAGCATGGCCCTATCAAAAATAAATGAGCGAAAGTCCCAATAAAACAGTATCTGAGGAAAA

      810     820     830     840     850     860     870     880
AGCTAAACAATACCTAGAAGAATTTTCATCAAAACGGCATTAGAGCATCCTGAATTGTCAGAACTTAAACCGTTACTGGGA

      890     900     910     920     930     940     950     960
CCAAATCCTGTATTTCGCTGGGGCTAACTATGCGGCGTGGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGAT

      970     980     990    1000    1010    1020    1030    1040
AATTTGGAAAAGACAACCTGCTGCTCTTTCGATACTTCTGGTATCGGTAGCGTAATGGGCATTGCAGACGGTGCCGTTCA

    1050    1060    1070    1080    1090    1100    1110    1120
CCACAATACAGAAGAGATAGTGGCACAATCAATAGCTTTATCGTCTTTAATGGTTGCTCAAGCTATTCCATTGGTAGGAG

    1130    1140    1150    1160    1170    1180    1190    1200
AGCTAGTTGATATTGGTTTCGCTGCATATAATTTGTAGAGAGTATTATCAATTTATTTCAAGTAGTTCATAATTCGTAT

    1210    1220    1230    1240    1250    1260    1270    1280
AATCGTCCCGCTATTCTCCGGGGCATAAAACGCAACCATTTCTTCATGACGGGTATGCTGTCAGTTGGAACACTGTTGA

    1290    1300    1310    1320    1330    1340    1350    1360
AGATTCGATAATCCGAACTGGTTTCAAGGGGAGAGTGGGCACGACATAAAAATTACTGCTGAAAAATACCCCGCTTCAA

    1370    1380    1390    1400    1410    1420    1430    1440
TCGCGGGTGTCTACTACCGACTATTCTCGGAAAGCTGGACGTTAATAAGTCCAAGACTCATATTTCCGTAATGGTGGG

    1450    1460    1470    1480    1490    1500    1510    1520
AAAAAAGGATGCGTTGCAGAGCTATAGACGGTGATGTAACCTTTTGTGCGCCCTAAATCTCCTGTTATGTTGGTAATGG

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Table 1 (continued)

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1530 1540 1550 1560 1570 1580 1590 1600
 TGTGCATGCTAACCTGTTTCGAACAGTTTCCCAATTAACAAGAGAAATTTATACAAACCCAGTATTAGAAAATTTTGATG
 10 1610 1620 1630 1640 1650 1660 1670 1680
 GTAGTTTTCGAGGCTCGGCTCAGGGCATAGAAAGAAGTATTAGGAGTCCACATTTGATGGATATACTTAACAGTATAACC
 1690 1700 1710 1720 1730 1740 1750 1760
 ATCTATACGGATGCTCATAGGGTTATTATTATTGGTTCAGGGCATCAAATAATGGCTTCTCCTGTAGGGTTTTCGGGGCC
 15 1770 1780 1790 1800 1810 1820 1830 1840
 AGAATTCACCTTTTCCGCTATATGCAACTATGGGAAATGCAGCTCCACAACAACGTATTGTTGCTCAACTAGGTCAGGGCG
 1850 1860 1870 1880 1890 1900 1910 1920
 TGTATAGAACATTATCGTCCACTTTATATAGAAGACCTTTTAATATAGGGATAAATAATCAACAACATCTGTTCTTGAC
 1930 1940 1950 1960 1970 1980 1990 2000
 20 GGGACAGAATTTGCTTATGGAACTCCTCAAATTTGCCATCCGCTGTATACAGAAAAAGCGGAACGGTAGATTGCTGGGA
 2010 2020 2030 2040 2050 2060 2070 2080
 TGAAATACCGCCACAGAATAACAACGTGCCACCTAGGCAAGGATTTAGTCATCGATTAAGCCATGTTTCAATGTTTCGTT
 2090 2100 2110 2120 2130 2140 2150 2160
 25 CAGGCTTTAGTAATAGTAGTGAAGTATAATAAGAGCTCCTATGTTCTCTTGGATACATCGTAGTGCTGAATTTAATAAT
 2170 2180 2190 2200 2210 2220 2230 2240
 ATAATTGCATCGGATAGTATTAATAATCCCTGCAGTGAAGGGAAACTTTCTTTTAAATGGTTCTGTAATTTTCAGGACC
 2250 2260 2270 2280 2290 2300 2310 2320
 AGGATTTACTGGTGGGACTTAGTTAGATTAAATAGTAGTTCGAAATAACATTTCAGAAATAGAGGGTATATTGAAGTTCCAA
 23 2330 2340 2350 2360 2370 2380 2390 2400
 TTCACTTCCCATCGACATCTACCAGATATCGAGTTCGTGTACGGTATGCTTCTGTAACCCCGATTACCTCAACGTTAAT
 2410 2420 2430 2440 2450 2460 2470 2480
 TGGGGTAATTCATCCATTTTTCCAATACAGTACCAGCTACAGCTACGTCATTAGATAATCTACAATCAAGTGATTTGG
 2490 2500 2510 2520 2530 2540 2550 2560
 35 TTATTTTGAAAGTCGCAATGCTTTTACATCTTCATTAGGTAATATAGTAGGTGTTAGAAATTTTAGTGGGACTGCAGGAG
 2570 2580 2590 2600 2610 2620
 TGATAATAGACAGATTGAATTTATCCAGTTACTGCAACACTCGAGTAGTAGGTTCGACAGCTT

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Table 2. DNA encoding quarter-length hybrid toxin

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10 20 30 40 50 60 70 80
 GTGAGCAGAAAACTGTTTGGCGTCAATCTTAATAGGGGCGCTACTGGGGATAGGGGCCCCACCTTCAGCCCATGCAGGCGC
 90 100 110 120 130 140 150 160
 TGATGATGTTGTTGATTCTTCTAAATCTTTGTGATGAAAACTTTCTTCGTACCACGGGACTAAACCTGGTTATGTAG
 170 180 190 200 210 220 230 240
 ATTCCATTCAAAAAGGTATACAAAAGCCAAAATCTGGTACACAAGGAATTATGACGATGATTGGAAGGGTTTATAGT
 250 260 270 280 290 300 310 320
 ACCGACAATAAATACGACGCTGCGGGATACTCTGTAGATAATGAAAAACCGCTCTCTGGAAAAGCTGGAGGCGTGGTGAA
 330 340 350 360 370 380 390 400
 AGTGACGTATCCAGGACTGACGAAGGTTCTCGCACTAAAAAGTGGATAATGCCGAACTATTAAGAAAGAGTTAGGTTTAA
 410 420 430 440 450 460 470 480
 GTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTTATCAAAAGGTTGCGTGATGGTGCTTCGCGTGTAGTG
 490 500 510 520 530 540 550 560
 CTCAGCCTTCCCTTCGCTGAGGGGAGTTCTAGCGTTGAATATATTAATAACTGGGAACAGGCGAAAGCGTTAAGCGTAGA
 570 580 590 600 610 620 630 640
 ACTTGAGATTAATTTTGAACCCGTGGAAAACGTGGCCAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAA
 650 660 670 680 690 700 710 720
 ATCGTGTGACGGCGATCAGTAGGTAGCTCATTGTGTCATGATAAATCTTGATTGGGATGTCATAGGGATAAACTAAGACA
 730 740 750 760 770 780 790 800
 AAGATAGAGTCTTTGAAAGAGCATGGCCCTATCAAAAATAAATGAGCGAAAGTCCCAATAAAACAGTATCTGAGGAAAA
 810 820 830 840 850 860 870 880
 AGCTAAACAATACCTAGAAGAATTTCATCAACGGCATTAGAGCATCCTGAATTGTCAGAACCTAAACCGTTACTGGGA
 890 900 910 920 930 940 950 960
 CCAATCCTGTATTCTGCTGGGGCTAACTATGCGGCGTGGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGAT
 970 980 990 1000 1010 1020 1030 1040
 AATTTGGAAAAGACAACCTGCTGCTCTTTCGATACTTCTCTGGTATCGGTAGCGTAATGGGCATTGACAGACGGTCCGTTCA
 1050 1060 1070 1080 1090 1100 1110 1120
 CCACAATACAGAAGAGATAGTGGCACAATCAATAGCITTATCGTCTTTAATGGTTGCTCAAGCTATTCCATTGGTAGGAG
 1130 1140 1150 1160 1170 1180 1190 1200
 AGCTAGTTGATATTGGTTTCGCTGCATATAATTTGTAGAGAGTATTATCAATTTATTTCAAGTAGTTTCAATTCGTAT
 1210 1220 1230 1240 1250 1260 1270 1280
 AATCGTCCCGGTATTCTCCGGGGCATAAAACGCAACCAATTTCTTCATGACGGGTATGCTGTGCTGAGTTGGAACACTGTGA
 1290 1300 1310 1320 1330 1340 1350 1360
 AGATTGATAATCCGAACCTGGTTTCAAGGGGAGAGTGGGCACGACATAAAAAATTACTGCTGAAAAATACCCCGCTTCCAA
 1370 1380 1390 1400 1410 1420 1430 1440
 TCGCGGGTGTCTACTACCGACTATTCTGGAAGCTGGACGTTAATAAGTCCAAGACTCATATTTCCGTAAATGGTTCGG
 1450 1460 1470 1480 1490 1500 1510 1520
 AAAATAAGGATGCGTTGCAGAGCTATAGACGGTGATGTAACCTTTTGTGCGCCCTAAATCTCTGTTTATGTTGGTAATGG

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Table 2 (continued)

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	1530	1540	1550	1560	1570	1580	1590	1600
	TGTGCATGCAGGTGCAGCTCCTATGTTCTCTTGGATACATCGTAGTGCCTGAATTTAATAATATAATTGCATCGGATAGTA							
10	1610	1620	1630	1640	1650	1660	1670	1680
	TTACTCAAATCCCTGCAGTGAAGGGAACTTTCTTTTAATGGTTCTGTAATTCAGGACCAGGATTTACTGGTGGGGAC							
	1690	1700	1710	1720	1730	1740	1750	1760
	TTAGTTAGATTAAATAGTAGTCCGAAATAACATTCAGAATAGAGGGTATATTGAAGTTCCAATTCACCTCCCATCGACATC							
15	1770	1780	1790	1800	1810	1820	1830	1840
	TACCAGATATCGAGTTCGTGTACGGTATGCTTCTGTAAACCCGATTACCTCAACGTTAATTGGGGTAATTCATCCATTT							
	1850	1860	1870	1880	1890	1900	1910	1920
	TTTCCAATACAGTACCAGCTACAGCTACGTCATTAGATAATCTACAATCAAGTGATTTTGGTTATTTGAAAGTCGCAAT							
	1930	1940	1950	1960	1970	1980	1990	2000
	GCTTTTACATCTTCATTAGGTAATATAGTAGGCTCTTAGAAATTTTGTAGTGGGACTGCAGGAGTGATAATAGACAGATTGGA							
20	2010	2020	2030	2040				
	ATTTATTCCAGTTACTGCAACACTCGAGTAGTAGGTCGACAGCTT							

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Table 3. Amino acid sequence of half-length hybrid toxin

	1	M	S	R	K	L	F	A	S	I	L	I	G	A	L	L	G	I	G	A	P	P	S	A	H	A	G	A	D	D	V		
	31	V	D	S	S	K	S	F	V	M	E	N	F	S	S	Y	H	G	T	K	P	G	Y	V	D	S	I	Q	K	G	I		
	61	Q	K	P	K	S	G	T	Q	G	N	Y	D	D	D	W	K	G	F	Y	S	T	D	N	K	Y	D	A	A	G	Y		
30	91	S	V	D	N	E	N	P	L	S	G	K	A	G	G	V	V	K	V	T	Y	P	G	L	T	K	V	L	A	L	K		
	121	V	D	N	A	E	T	I	K	K	E	L	G	L	S	L	P	F	A	E	G	S	S	S	V	E	Y	I	N	N	W	E	Q
	151	R	F	G	D	G	A	S	R	V	V	L	S	L	P	F	A	E	G	S	S	S	S	V	E	Y	I	N	N	W	E	Q	
	181	A	K	A	L	S	V	E	L	E	I	N	F	E	T	R	G	K	R	G	Q	D	A	M	Y	E	Y	M	A	Q	A	T	
	211	C	A	G	N	R	V	R	R	S	V	G	S	S	L	S	C	I	N	L	D	W	D	V	I	R	D	K	T	K	T	G	
	241	K	I	E	S	L	K	E	H	G	P	I	K	N	K	M	S	E	S	P	N	K	T	V	S	E	E	K	A	K	Q	G	
35	271	Y	L	E	E	F	H	Q	T	A	L	E	H	P	E	L	S	E	L	K	T	V	T	G	T	N	P	V	F	A	G	S	
	301	A	N	Y	A	A	W	A	V	N	V	A	Q	V	I	D	S	E	T	A	D	N	L	E	K	T	T	A	A	L	S		
	331	I	L	P	G	I	G	S	V	M	G	I	A	D	G	A	V	H	H	N	T	E	E	I	V	A	Q	S	I	A	L		
	361	S	S	L	M	V	A	Q	A	I	P	L	V	G	E	L	V	D	I	G	F	A	A	Y	N	F	V	E	S	I	I		
	391	N	L	F	Q	V	V	H	N	S	Y	N	R	P	A	Y	S	P	G	H	K	T	Q	P	F	L	H	D	G	Y	A		
	421	V	S	W	N	T	V	E	D	S	I	I	R	T	G	F	Q	G	E	S	G	H	D	I	K	I	T	A	E	N	T		
40	451	P	L	P	I	A	G	V	L	L	P	T	I	P	G	K	L	D	V	N	K	S	K	T	H	I	S	V	N	G	R		
	481	K	I	R	M	R	C	R	A	I	D	G	D	V	T	F	C	R	P	K	S	P	V	Y	V	G	N	G	V	H	A		
	511	N	L	F	R	T	V	S	Q	L	T	R	E	I	Y	T	N	P	V	L	E	N	F	D	G	S	F	R	G	S	A		
	541	Q	G	I	E	R	S	I	R	S	P	H	L	M	D	I	L	N	S	I	T	I	Y	T	D	A	H	R	G	Y	Y		
	571	Y	W	S	G	H	Q	I	M	A	S	P	V	G	F	S	G	P	E	F	T	F	P	L	Y	G	T	M	G	N	A		
45	601	A	P	Q	Q	R	I	V	A	Q	L	G	Q	G	V	Y	R	T	L	S	S	T	L	Y	R	R	P	F	N	I	G		
	631	I	N	N	Q	Q	L	S	V	L	D	G	T	E	F	A	Y	G	T	S	S	N	L	P	S	A	V	Y	R	K	S		
	661	G	T	V	D	S	L	D	E	I	P	P	Q	N	N	N	V	P	P	R	Q	G	F	S	H	R	L	S	H	V	S		
	691	M	F	R	S	G	F	S	N	S	S	V	S	I	I	R	A	P	M	F	S	W	I	H	R	S	A	E	F	N	N		
	721	I	I	A	S	D	S	I	T	Q	I	P	A	V	K	G	N	F	L	F	N	G	S	V	I	S	G	P	G	F	T		
	751	G	G	D	L	V	R	L	N	S	S	G	N	N	I	Q	N	R	G	Y	I	E	V	P	I	H	F	P	S	T	S		
50	781	T	R	Y	R	V	R	V	R	Y	A	S	V	T	P	I	H	L	N	V	N	W	G	N	S	S	I	F	S	N	T		
	811	V	P	A	T	A	T	S	L	D	N	L	Q	S	S	D	F	G	Y	F	E	S	A	N	A	F	T	S	S	L	G		
	841	N	I	V	G	V	R	N	F	S	G	T	A	G	V	I	I	D	R	F	E	F	I	P	V	T	A	T	L	E			
	871																																

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The one-letter symbol for the amino acids used in Tables 3 and 4 is well known in the art. For convenience, the relationship of the three-letter abbreviation and the one-letter symbol for amino acids is as follows:

Ala	A	Leu	L
Arg	R	Lys	K
Asn	N	Met	M
Asp	D	Phe	F
Cys	C	Pro	P
Gln	Q	Ser	S
Glu	E	Thr	T
Gly	G	Trp	W
His	H	Tyr	Y
Ile	I	Val	V

Table 4. Amino acid sequence of quarter-length hybrid toxin

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1  MSRKLFASILIGALLGIGAPPSSAHAGADDV
31  VDS SKS FVMENFSSYHGTPGYVDSIQKGI
61  QKPKSGTQGGNYDDDDWKGFYSTDNKYDAAGY
91  SVDNENPLSGKAGGVVKVTYPGLTKVLALK
121 VDNAETIKKELGLSLTEPLMEQVGT EEFIK
151 RFGDGA SRV VLSLPFAEGSSSVEYINNWEQ
181 AKALSVELEINFETRGRGQDAMY EYMAQA
211 CAGNRVRRSVGSSSLSCINLDWDVIRDKTKT
241 KIESLKEHGP IKNKMSESPNTVSEEEKAKQ
271 YLEEFHQTALEHPELSELKTVTGTNPVFAG
301 ANYAAWAVNV AQVIDSETADNLEKTTAALS
331 ILPGIGSVMG IADGAVHHNT EEIVAQSI AL
361 SSLMVAQAIP LVGELVDIGFAAYNFVESII
391 NLFQVVHNSYNRPAYSPGHKTQPF LHDGYA
421 VSWNTVEDS IIRTFGFGESGHD IKITAENT
451 PLPIAGVLLPTIPGKL DVNKS SKTHISVNGR
481 KIRMRRCRAIDG DVTFCRPKSPVYVGN GVHA
511 GAAPMF SWIHRSAEFNNIIASDSITQIPAV
541 KGNFLFNGSVISGPGFTGGDLVRLNSSSGNN
571 IQNRGYIEVP IHF PSTSTRYRVRVRYASVT
601 PIHLNVNWGNS SIFSNTPATATSLDNLQS
631 SDFGYFESANAFTSSLGNIVGV RNFS GTAG
661 V I I D R F E F I P V T A T L E
691

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Table 5

Relative molecular weights of polypeptides present in SeNPV and HzNPV LOVAL preparations as determined by SDS-polyacrylamide gel electrophoresis.		
STANDARDS	LOVAL	
	SeNPV	HzNPV
205,000 -----	>205,000	
97,000 -----		
	85,000	90,000
	72,000	76,000
		68,000
66,000 -----		
	62,000	65,000
	55,000	51,000
	50,000	46,000
45,000 -----	45,000	45,000
	42,000	40,000
		38,000
36,000 -----		
	34,000	34,000
	33,000	
	30,000	30,000
29,000 -----	29,000	
	25,000	25,000
24,000 -----	<24,000	<24,000
The polypeptides present in SeNPV and HzNPV LOVAL preparations were separated by polyacrylamide gel electrophoresis (7.5%) in the presence of SDS as described (Laemmli, U.K., [1970] Nature [London] 227:680-685).		

Table 6

Hybrid virus infectivity				
Number of Larvae Dead per 24 at 7 Days Post-Infection				
LARVAE	VIRUS			Buffer
	SeNPV	HzNPV	Se*HzNPV	
<i>S. exigua</i>	24	9	19	1
<i>H. zea</i>	4	23	21	6

LOVAL was suspended in buffer containing 40 mM Tris-acetate, 1 mM EDTA, pH 8.0 (TAE). Octyl glucoside was added at a ratio of 1:2 (w/w) and the mixture was incubated for 4 hours at 37°C with constant shaking at 200 rpm. Non-solubilized viral protein was removed by centrifugation at 100,000 g for 1 hr at 4°C. The supernatant was dialyzed with HzNPV LOVAL at a ratio of 1:1 (w/w) for 24 hours against 3 changes of TAE buffer. The dialysate was centrifuged at 100,000 g for 1 hr at 4°C. The supernatant was discarded and the pellet containing the hybrid virus (Se*HzNPV) was resuspended in TAE buffer to be used in bioassay or for analysis by SDS-PAGE.

Table 7

Relative molecular weights.		
STANDARDS	SOLUBILIZED SeNPV	HYBRID VIRUS Se*HzNPV
205,000 -----		
97,000 -----		
66,000 -----		
45,000 -----	50,000	50,000
	43,000	43,000
	38,000	38,000
36,000 -----		
29,000 -----		
24,000 -----		

In order to determine which of the three polypeptides extracted by octyl glucoside solubilization of SeNPV was responsible for conferring virulence to the NzHPV hybrid virus (Se*HzNPV) to *Spodoptera exigua* the following experiment was performed: The three SeNPV proteins extracted by octyl glucoside were labeled with ¹²⁵I. The hybrid virus was prepared as described using the radiolabeled proteins and unlabeled HzNPV. An autoradiogram of an SDS-polyacrylamide gel of the hybrid virus showed all three proteins to be associated with HzNPV.

Brief Description of the Drawings

FIGURE 1: Partial restriction endonuclease map of MR436 coding sequence.

FIGURE 2: HD-73 toxin binding to CF-1 cells. Cells were incubated with the indicated concentrations of unlabeled HD-73 for 20 minutes, then with radiolabeled toxin for an additional 30 minutes. Bound radioactivity was determined as described in Materials and Methods.

FIGURE 3: CNBr peptide competition with radioiodinated HD-73 for binding to CF-1 cells. HD-73 toxin was digested with CNBr and dialyzed. CF-1 cells were incubated with the indicated concentrations of the digest peptides for 20 minutes, then with radioiodinated HD-73 toxin for an additional 30 minutes. Bound radioactivity was determined as described in Materials and Methods.

FIGURE 4: Diphtheria toxin-catalyzed ADP-Ribosylation of EF-2. Partially purified EF-2 from wheat germ was incubated with the indicated concentrations of diphtheria toxin for 10 minutes, then with ¹⁴C-NAD for an additional 30 minutes at 37° C. The reaction was terminated by the addition of cold TCA, and the precipitated protein was recovered and counted for radioactivity as described in Materials and Methods. The extents of ribosylation are expressed as a percentage of that obtained with saturating concentrations of diphtheria toxin.

FIGURE 5: Hybrid toxin-catalyzed ribosylation of EF-2. Wheat germ EF-2 was incubated with quarter (□) or half length (Δ) hybrid toxins at the indicated concentrations for 10 minutes, then with ¹⁴C-NAD for 30 minutes. Samples were processed as described for Figure 3. Ribosylation is expressed as a percentage of that obtained with a saturating concentration of diphtheria toxin.

FIGURE 6: Inhibition of protein synthesis in CF-1 cells by HD-73 toxin. Cells were incubated with the indicated concentrations of toxin for 20 minutes, then assayed for incorporation of ¹⁴C-leucine into protein as described in Materials and Methods. Results are expressed as a percentage of that obtained for CF-1 cells in the absence of toxin.

FIGURE 7: Inhibition of protein synthesis in CF-1 cells by hybrid toxins. Cells were exposed to quarter or half length hybrid toxins for 1 or 24 hours, the assayed for ¹⁴C-leucine incorporation into protein as described in Materials and Methods. Percentage inhibition of protein synthesis was determined by comparison to control cells which were incubated for identical time intervals in the absence of hybrid toxins.

Detailed Description of the Invention

Novel hybrid toxins are produced by fusion of a pesticidal toxin to a cytotoxic agent. Specifically exemplified herein is a hybrid B.t. toxin prepared by fusion of the insect gut epithelial cell recognition region of a B.t. gene to diphtheria toxin B chain.

The hybrid toxin gene of the subject invention can be introduced into a wide variety of microbial hosts. Expression of the toxin gene results, directly or indirectly, in the intracellular production and maintenance of the pesticide. With suitable hosts, e.g., *Pseudomonas*, the microbes can be applied to the situs of coleopteran insects where they will proliferate and be ingested by the insects. The result is a control of the unwanted insects. Alternatively, the microbe hosting the toxin gene can be treated under conditions that prolong the activity of the toxin produced in the cell. The treated cell then can be applied to the environment of target pest(s). The resulting product retains the toxicity of the B.t. toxin.

Where the B.t. toxin gene is introduced via a suitable vector into a microbial host, and said host is applied to the environment in a living state, it is essential that certain host microbes be used. Microorganism hosts are selected which are known to occupy the "phytosphere" (phylloplane, phyllosphere, rhizosphere, and/or rhizoplane) of one or more crops of interest. These microorganisms are selected so as to be capable of successfully competing in the particular environment (crop and other insect habitats) with the wild-type microorganisms, provide for stable maintenance and expression of the gene expressing the polypeptide pesticide, and, desirably, provide for improved protection of the pesticide from environmental degradation and inactivation.

A large number of microorganisms are known to inhabit the phylloplane (the surface of the plant leaves) and/or the rhizosphere (the soil surrounding plant roots) of a wide variety of important crops. These microorganisms include bacteria, algae, and fungi. Of particular interest are microorganisms, such as bacteria, e.g., genera *Pseudomonas*, *Erwinia*, *Serratia*, *Klebsiella*, *Xanthomonas*, *Streptomyces*, *Rhizobium*, *Rhodopseudomonas*, *Methylophilus*, *Agrobacterium*, *Acetobacter*, *Lactobacillus*, *Arthrobacter*, *Azotobacter*, *Leuconostoc*, and *Alcaligenes*; fungi, particularly yeast, e.g., genera *Saccharomyces*, *Cryptococcus*, *Kluyveromyces*, *Sporobolomyces*, *Rhodotorula*, and *Aureobasidium*. Of particular interest are such phytosphere bacterial species as *Pseudomonas syringae*, *Pseudomonas fluorescens*, *Serratia marcescens*, *Acetobacter xylinum*, *Agrobacterium tumefaciens*, *Rhodopseudomonas spheroides*, *Xanthomonas campestris*, *Rhizobium meliloti*, *Alcaligenes entrophus*, and *Azotobacter vinlandii*; and phytosphere yeast species such as *Rhodotorula rubra*, *R. glutinis*, *R. marina*, *R. aurantiaca*, *Cryptococcus albidus*, *C. diffluens*, *C. laurentii*, *Saccharomyces rosei*, *S. pretoriensis*, *S. cerevisiae*, *Sporobolomyces roseus*, *S. odoratus*, *Kluyveromyces veronae*, and *Aureobasidium pollulans*. Of particular interest are the pigmented microorganisms.

A wide variety of ways are available for introducing the B.t. gene expressing the toxin into the microorganism host under conditions which allow for stable maintenance and expression of the gene. One can provide for DNA constructs which include the transcriptional and translational regulatory signals for expression of the toxin gene, the toxin gene under their regulatory control and a DNA sequence homologous with a sequence in the host organism, whereby integration will occur, and/or a replication system which is functional in the host, whereby integration or stable maintenance will occur.

The transcriptional initiation signals will include a promoter and a transcriptional initiation start site. In some instances, it may be desirable to provide for regulative expression of the toxin, where expression of the toxin will only occur after release into the environment. This can be achieved with operators or a region binding to an activator or enhancers, which are capable of induction upon a change in the physical or chemical environment of the microorganisms. For example, a temperature sensitive regulatory region may be employed, where the organisms may be grown up in the laboratory without expression of a toxin, but upon release into the environment, expression would begin. Other techniques may employ a specific nutrient medium in the laboratory, which inhibits the expression of the toxin, where the nutrient medium in the environment would allow for expression of the toxin. For translational initiation, a ribosomal binding site and an initiation codon will be present.

Various manipulations may be employed for enhancing the expression of the messenger, particularly by using an active promoter, as well as by employing sequences, which enhance the stability of the messenger RNA. The initiation and translational termination region will involve stop codon(s), a terminator region, and optionally, a polyadenylation signal.

In the direction of transcription, namely in the 5' to 3' direction of the coding or sense sequence, the construct will involve the transcriptional regulatory region, if any, and the promoter, where the regulatory region may be either 5' or 3' of the promoter, the ribosomal binding site, the initiation codon, the structural gene having an open reading frame in phase with the initiation codon, the stop codon(s), the polyadenylation

tion signal sequence, if any, and the terminator region. This sequence as a double strand may be used by itself for transformation of a microorganism host, but will usually be included with a DNA sequence involving a marker, where the second DNA sequence may be joined to the toxin expression construct during introduction of the DNA into the host.

5 By a marker is intended a structural gene which provides for selection of those hosts which have been modified or transformed. The marker will normally provide for selective advantage, for example, providing for biocide resistance, e.g., resistance to antibiotics or heavy metals; complementation, so as to provide prototrophy to an auxotrophic host, or the like. Preferably, complementation is employed, so that the modified host may not only be selected, but may also be competitive in the field. One or more markers
10 may be employed in the development of the constructs, as well as for modifying the host. The organisms may be further modified by providing for a competitive advantage against other wild-type microorganisms in the field. For example, genes expressing metal chelating agents, e.g., siderophores, may be introduced into the host along with the structural gene expressing the toxin. In this manner, the enhanced expression of a siderophore may provide for a competitive advantage for the toxin-producing host, so that it may effectively
15 compete with the wild-type microorganisms and stably occupy a niche in the environment.

Where no functional replication system is present, the construct will also include a sequence of at least 50 basepairs (bp), preferably at least about 100 bp, and usually not more than about 1000 bp of a sequence homologous with a sequence in the host. In this way, the probability of legitimate recombination is enhanced, so that the gene will be integrated into the host and stably maintained by the host. Desirably, the
20 toxin gene will be in close proximity to the gene providing for complementation as well as the gene providing for the competitive advantage. Therefore, in the event that a toxin gene is lost, the resulting organism will be likely to also lose the complementing gene and/or the gene providing for the competitive advantage, so that it will be unable to compete in the environment with the gene retaining the intact construct.

25 A large number of transcriptional regulatory regions are available from a wide variety of microorganism hosts, such as bacteria, bacteriophage, cyanobacteria, algae, fungi, and the like. Various transcriptional regulatory regions include the regions associated with the *trp* gene, *lac* gene, *gal* gene, the lambda left and right promoters, the Tac promoter, the naturally-occurring promoters associated with the toxin gene, where functional in the host. See for example, U.S. Patent Nos. 4,332,898, 4,342,832 and 4,356,270. The
30 termination region may be the termination region normally associated with the transcriptional initiation region or a different transcriptional initiation region, so long as the two regions are compatible and functional in the host.

Where stable episomal maintenance or integration is desired, a plasmid will be employed which has a replication system which is functional in the host. The replication system may be derived from the
35 chromosome, an episomal element normally present in the host or a different host, or a replication system from a virus which is stable in the host. A large number of plasmids are available, such as pBR322, pACYC184, RSF1010, pR01614, and the like. See for example, Olson et al., (1982) J. Bacteriol. 150:6069, and Bagdasarian et al., (1981) Gene 16:237, and U.S. Patent Nos. 4,356,270, 4,362,817, and 4,371,625.

The B.t. gene can be introduced between the transcriptional and translational initiation region and the
40 transcriptional and translational termination region, so as to be under the regulatory control of the initiation region. This construct will be included in a plasmid, which will include at least one replication system, but may include more than one, where one replication system is employed for cloning during the development of the plasmid and the second replication system is necessary for functioning in the ultimate host. In addition, one or more markers may be present, which have been described previously. Where integration is
45 desired, the plasmid will desirably include a sequence homologous with the host genome.

The transformants can be isolated in accordance with conventional ways, usually employing a selection technique, which allows for selection of the desired organism as against unmodified organisms or transferring organisms, when present. The transformants then can be tested for pesticidal activity.

Suitable host cells, where the pesticide-containing cells will be treated to prolong the activity of the
50 toxin in the cell when the then treated cell is applied to the environment of target pest(s), may include either prokaryotes or eukaryotes, normally being limited to those cells which do not produce substances toxic to higher organisms, such as mammals. However, organisms which produce substances toxic to higher organisms could be used, where the toxin is unstable or the level of application sufficiently low as to avoid any possibility of toxicity to a mammalian host. As hosts, of particular interest will be the prokaryotes and
55 the lower eukaryotes, such as fungi. Illustrative prokaryotes, both Gram-negative and -positive, include Enterobacteriaceae, such as *Escherichia*, *Erwinia*, *Shigella*, *Salmonella*, and *Proteus*; Bacillaceae; Rhizobiaceae, such as *Rhizobium*; Spirillaceae, such as *Photobacterium*, *Zymomonas*, *Serratia*, *Aeromonas*, *Vibrio*, *Desulfovibrio*, *Spirillum*; Lactobacillaceae; Pseudomonadaceae, such as *Pseudomonas* and *Aceto-*

bacter; Azotobacteraceae and Nitrobacteraceae. Among eukaryotes are fungi, such as Phycomycetes and Ascomycetes, which includes yeast, such as Saccharomyces and Schizosaccharomyces; and Basidiomycetes yeast, such as Rhodotorula, Aureobasidium, Sporobolomyces, and the like.

Characteristics of particular interest in selecting a host cell for purposes of production include ease of introducing the B.t. gene into the host, availability of expression systems, efficiency of expression, stability of the pesticide in the host, and the presence of auxiliary genetic capabilities. Characteristics of interest for use as a pesticide microcapsule include protective qualities for the pesticide, such as thick cell walls, pigmentation, and intracellular packaging or formation of inclusion bodies; leaf affinity; lack of mammalian toxicity; attractiveness to pests for ingestion; ease of killing and fixing without damage to the toxin; and the like. Other considerations include ease of formulation and handling, economics, storage stability, and the like.

Host organisms of particular interest include yeast, such as Rhodotorula sp., Aureobasidium sp., Saccharomyces sp., and Sporobolomyces sp.; phylloplane organisms such as Pseudomonas sp., Erwinia sp. and Flavobacterium sp.; or such other organisms as Escherichia, Lactobacillus sp., Bacillus sp., and the like. Specific organisms include Pseudomonas aeruginosa, Pseudomonas fluorescens, Saccharomyces cerevisiae, Bacillus thuringiensis, Escherichia coli, Bacillus subtilis, and the like.

The cell will usually be intact and be substantially in the proliferative form when treated, rather than in a spore form, although in some instances spores may be employed.

Treatment of the microbial cell, e.g., a microbe containing the B.t. toxin gene, can be by chemical or physical means, or by a combination of chemical and/or physical means, so long as the technique does not deleteriously affect the properties of the toxin, nor diminish the cellular capability in protecting the toxin. Examples of chemical reagents are halogenating agents, particularly halogens of atomic no. 17-80. More particularly, iodine can be used under mild conditions and for sufficient time to achieve the desired results. Other suitable techniques include treatment with aldehydes, such as formaldehyde and glutaraldehyde; anti-infectives, such as zephiran chloride and cetylpyridinium chloride; alcohols, such as isopropyl and ethanol; various histologic fixatives, such as Bouin's fixative and Helly's fixative (See: Humason, Gretchen L., Animal Tissue Techniques, W.H. Freeman and Company, 1967); or a combination of physical (heat) and chemical agents that preserve and prolong the activity of the toxin produced in the cell when the cell is administered to the host animal. Examples of physical means are short wavelength radiation such as gamma-radiation and X-radiation, freezing, UV irradiation, lyophilization, and the like.

The cells generally will have enhanced structural stability which will enhance resistance to environmental conditions. Where the pesticide is in a proform, the method of inactivation should be selected so as not to inhibit processing of the proform to the mature form of the pesticide by the target pest pathogen. For example, formaldehyde will crosslink proteins and could inhibit processing of the proform of a polypeptide pesticide. The method of inactivation or killing retains at least a substantial portion of the bio-availability or bioactivity of the toxin.

The cellular host containing the B.t. insecticidal gene may be grown in any convenient nutrient medium, where the DNA construct provides a selective advantage, providing for a selective medium so that substantially all or all of the cells retain the B.t. gene. These cells may then be harvested in accordance with conventional ways. Alternatively, the cells can be treated prior to harvesting.

The B.t. cells may be formulated in a variety of ways. They may be employed as wettable powders, granules or dusts, by mixing with various inert materials, such as inorganic minerals (phyllosilicates, carbonates, sulfates, phosphates, and the like) or botanical materials (powdered corncobs, rice hulls, walnut shells, and the like). The formulations may include spreader-sticker adjuvants, stabilizing agents, other pesticidal additives, or surfactants. Liquid formulations may be aqueous-based or non-aqueous and employed as foams, gels, suspensions, emulsifiable concentrates, or the like. The ingredients may include rheological agents, surfactants, emulsifiers, dispersants, or polymers.

The pesticidal concentration will vary widely depending upon the nature of the particular formulation, particularly whether it is a concentrate or to be used directly. The pesticide will be present in at least 1% by weight and may be 100% by weight. The dry formulations will have from about 1-95% by weight of the pesticide while the liquid formulations will generally be from about 1-60% by weight of the solids in the liquid phase. The formulations will generally have from about 10^2 to about 10^4 cells/mg. These formulations will be administered at about 50 mg (liquid or dry) to 1 kg or more per hectare.

The formulations can be applied to the environment of the coleopteran pest(s), e.g., plants, soil or water, by spraying, dusting, sprinkling, or the like.

Following are examples which illustrate procedures, including the best mode, for practicing the invention. These examples should not be construed as limiting. All percentages are by weight and all solvent mixture proportions are by volume unless otherwise noted.

The adapters regenerate the SphI site, eliminate the NsiI site, maintain the correct translation reading frame, and add two amino acids (ala-gly) between diphtheria toxin B-chain his⁴⁸⁴ and HD-73 cys¹⁰. The details of the fusion junction, with the adapters boxed, are shown below:

diphtheria toxin HD-73
B-chain

50

HD-73

pBC508

09/28/2004, EAST Version: 1.4.1

The correct translational reading frame at the fusion junction between diphtheria toxin B-chain and HD-73 coding sequences was verified by dideoxy DNA sequencing of p26 using a synthetic oligonucleotide primer corresponding to nucleotides 500 to 523 of the diphtheria toxin gene (Murphy, J.R. [1985] Current Topics Microbiol. Immunol. 118:235-251):

5' - GACGGTGATGTAAC(TTTT)GTCTGC - 3'

Plasmid p26, described above, served as the substrate for additional hybrid toxin constructions. Two constructs were generated which either fuse His⁴⁸⁴ of diphtheria toxin B-chain to amino acids Arg²⁵⁸ through Glu⁶¹³ of HD-73 (plasmid construct p151), or His⁴⁸⁴ of diphtheria toxin B-chain to amino acid Ala⁴⁵⁰ through Glu⁶¹³ of HD-73 (plasmid construct p11). Hybrid toxin plasmid p151 was generated by restriction digestion of p26 with *Sph*I and *Asu*II, gel-purification of the DNA fragment containing pBC508 plus HD-73 coding for Arg²⁵⁸ through the synthetic *Xho*I-HindIII adaptor (described above), and re-ligation of the *Sph*I to the *Asu*II site with a synthetic oligonucleotide adaptor set of the sequence:

40 The adaptor set regenerates the SphI and AsuII sites, maintains the correct translational reading frame, and inserts four amino acids (Ala-Asn-Leu-Phe) between His⁴³⁴ of the diphtheria toxin B-chain and Arg²⁵⁸ of HD-73 coding sequence. Details of the predicted construct at the fusion junction, with the synthetic adaptors boxed, are shown below:

Recombinant plasmids were screened for the presence of the SphI site, and the correct size of the insert was demonstrated by agarose gel-sizing of EcoRI digested p26 and p151, and by double-digests

comparing p26 (AsuII x SaII) with p151 (SphI x SaII).

Correct translational reading frame at the fusion junction was verified by dideoxy DNA sequencing of p151 with the synthetic sequencing primer used for p26 (above) and with a second synthetic oligonucleotide sequencing primer which corresponds to nucleotides 479 to 499 of the diphtheria toxin structural gene (Murphy, J.R. [1985] *supra*):

5' - AGGATGCGTTGCAGAGCTATA - 3'

Hybrid toxin plasmid p11 was constructed by restriction digestion of p26 with SphI and SstII, gel-purification of the DNA fragment containing pBC508 plus HD-73 coding for Ala⁴⁵⁰ through the synthetic XhoI-HindIII adaptor (described above), and re-ligation of the SphI to the SstII site with a synthetic oligonucleotide adaptor set.

5' - CAGGTGCAGCT - 3'
3' - GTACGTCCACG - 5'

The adaptor set regenerates the SphI site, eliminates the SstII site, maintains the correct translational reading frame, and inserts three amino acids (Ala-Gly-Ala) between His⁴⁸⁴ of the diphtheria toxin B-chain and Ala⁴⁵⁰ of the HD-73 coding sequence. Detail of the predicted structure at the fusion junction, with synthetic oligonucleotides boxed are shown below:

	Gly	Val	His	Ala	Gly	Ala	Ala	Pro	7
5' . . .	GGT	GTG	CAT	GCA	GGT	GCA	GCT	CCT . . .	3'
3' . . .	CCA	CAC	GTA	CGT	CCA	CGT	CGA	GGA . . .	5'

diphtheria
toxin B-chain

HD-73

Recombinant plasmids were screened for the presence of the SphI site, and the correct size of the insert was demonstrated by agarose gel-sizing of EcoRI digests of p11 compared to p26, and by multi-enzyme digests comparing p11 with p26 as follows:

p26	p11
<u>Sph</u> I x <u>Sa</u> II x <u>Sst</u> II	<u>Sph</u> I x <u>Sa</u> II
<u>Sst</u> II x <u>Sa</u> II	<u>Sph</u> I x <u>Sa</u> II

Correct translational reading frame at the fusion junction was demonstrated by dideoxy DNA sequencing of p11 with the same two synthetic oligonucleotide primers used for p151.

Example 3 - Construction of Hybrid Toxin Expression Vectors Containing Fused Coding Sequences for Diphtheria Toxin A-Chain and Truncated B-Chain and HD-73

HD-73 coding sequence DNA fragments were excised from plasmids p26, p151, and p11 by digestion with SphI and SaII, and gel-purified. These gel-purified fragments were used for construction of a hybrid toxin expression vector containing diphtheria toxin A and B-chains and HD-73 coding sequences. Assembly of the hybrid toxin expression vector was done under BL-3 containment conditions. Plasmid pAB1508 was digested with SphI and SaII to remove interleukin-2 (IL-2) coding sequence DNA. The vector (minus IL-2) was gel-purified. Purified SphI x SaII HD-73 inserts were ligated separately to the purified SphI x SaII pAB1508 vector DNA. The ligation mixes were used to transform *E. coli* strain SY327 cells. Correctly assembled hybrid toxin plasmids were identified with Western blots by their ability to produce anti-HD-73 immunoreactive material under control of the constitutively utilized ptox promoter of the diphtheria toxin

gene. Synthesis of three size classes of immunoreactive material was detected. A hybrid toxin made with p26 *SphI* x *Sall* HD-73 DNA gave immunoreactive protein which migrated between the 116 kd and 180 kd protein standards (computer-generated molecular weight is about 126 kd). A hybrid toxin made with the p151 *SphI* x *Sall* HD-73 insert gave immunoreactive protein which migrated between the 84 kd and 116 kd protein standards (computer-predicted molecular weight is about 98 kd). A hybrid toxin made with the p11 *SphI* x *Sall* HD-73 insert DNA gave an immunoreactive protein which migrated between the 58 kd and 84 kd protein standards (computer-predicted molecular weight is about 76 kd).

10 Example 4 - Expression of Hybrid Toxins in *E. coli*

Under BL-3 containment conditions, *E. coli* cells were grown in LB medium (with or without ampicillin) overnight at 30° C. Cells were collected by centrifugation and treated by one of the following three methods:

(a) Whole cells were killed with ultraviolet irradiation and kept on ice.
 15 (b) Periplasmic protein extracts were prepared from whole cells. Cell pellets were resuspended in ice-cold buffer containing 20% sucrose/10 mM Tris-HCl, pH 8.0, 1 mM ethylenediaminetetraacetic acid (EDTA). A volume of cold buffer containing 1.5 mg/ml lysozyme, equal in volume to the volume used for resuspension, was added and incubation proceeded for 20 minutes at 4° C. Cells were removed by centrifugation and the supernatant containing the periplasmic proteins was sonicated and filtered through
 20 0.45 µm filters. Filtered extract was frozen. The majority of hybrid toxin molecules in this extract should lack the diphtheria toxin leader sequence (amino acids -1 to -25) (Murphy [1985] supra) which should be clipped during secretion into the periplasmic space (Murphy, John R., U.S. Patent No. 4,675,382).

(c) Whole-cell extracts were prepared by disruption with a French Press (French pressure cell-laboratory hydraulic press) as follows. Cell pellets were resuspended in ice-cold buffer containing 20% glycerol/50 mM Tris-HCl, pH 7.4/1mM EDTA/1 mM dithiothreitol (DTT)/approximately 1 mM phenylmethylsulfonyl fluoride (PMSF). Cells were disrupted twice with the French Press at 12,000 to 14,000 psi. Cell
 25 extracts were frozen. The hybrid toxins should be a mixed population of molecules with respect to the presence of the diphtheria toxin leader sequence (amino acids -1 to -25) since some molecules were likely not secreted.

30

Example 5 - Purification of Hybrid Toxin

35 An immunoabsorbent resin was constructed by coupling an equine polyclonal diphtheria toxin antibody (Connaught Laboratories, Swiftwater, PA) to cyanogen bromide (CNBr)-activated SEPHAROSE™ 4B (Pharmacia Fine Chemicals, Piscataway, NJ) by following the latter manufacturer's procedure. Briefly, 3 g of lyophilized CNBr-activated SEPHAROSE™ was cycled into and repeatedly washed with 1 mM HCl. The resulting swollen gel was then washed with coupling buffer (0.5 M NaCl and 0.1 M NaHCO₃, pH 8.3). An
 40 aliquot of the diphtheria toxin antibody corresponding to 60 mg was suspended in coupling buffer at a final concentration of 5 mg protein to 5 ml buffer. The SEPHAROSE™ and antibody solution were then combined and allowed to incubate at room temperature for 2 hours with end over end mixing. Following the incubation period, the resin was briefly centrifuged (1000 xg x 15 min) and the supernatant was removed. Residual unoccupied reactive groups on the resin matrix were blocked by the addition of 0.2 M glycine, pH
 45 8.0 and allowing to incubate as before. Finally, the immunoabsorbent was washed sequentially in high and low pH buffers (coupling buffer and a buffer comprised of 0.1 M NaCl and 0.1 M NaHCO₃, pH 4). This wash was repeated 4 times to ensure that ionically bound free ligand was removed. This procedure resulted in an overall coupling efficiency of 95%. The prepared immunoabsorbent contained 5.7 mg ligand per ml resin. The immunoabsorbent was pre-equilibrated with loading buffer (100 mM Tris-Cl, pH 7.4, 20% glycerol, 1 mM
 50 Na₂EDTA, 1 mM PMSF, 0.1% nonidet P-40 (NP-40) and 0.1 mM DTT) at 4° C prior to chromatography.

All of the following steps were performed at 4° C unless otherwise noted. The disrupted cell pellet containing the hybrid toxin was partially solubilized by the addition of NP-40 to a final concentration of 0.1% (v/v) to promote dissolution of hydrophobic aggregates. An aliquot of the partially solubilized material, corresponding to 50 mg total protein, was incubated with a slurry of the resin corresponding to 0.5 ml
 55 SEPHAROSE™ for 3 hr with end over end mixing. Non-specifically bound material was removed from the resin by repeatedly cycling it into wash buffer (100 mM Tris-Cl, pH 7.4, 20% glycerol, 0.2% NP-40 and 0.1% cholic acid). This was followed by successive washes in 0.1 M Tris-Cl to remove all traces of detergent. Finally, the hybrid toxin was eluted by a short incubation with 4 M guanidine-HCl in 0.1 M Tris-

Cl, pH 7.4. This fraction was then dialyzed exhaustively against a buffer containing 20 mM Tris-Cl, pH 7.4, 0.1 M NaCl and 0.25 mM reduced glutathione to promote proper refolding.

5 Example 6 - Insertion of Toxin Gene Into Plants

The novel genes coding for the novel insecticidal toxins, as disclosed herein, can be inserted into plant cells using the Ti plasmid from *Agrobacter tumefaciens*. Plant cells can then be caused to regenerate into plants (Zambryski, P., Joos, H., Gentello, C., Leemans, J., Van Montague, M. and Schell, J [1983] Cell 32:1033-1043). A particularly useful vector in this regard is pEND4K (Klee, H.J., Yanofsky, M.F. and Nester, E.W. [1985] Bio/Technology 3:637-642). This plasmid can replicate both in plant cells and in bacteria and has multiple cloning sites for passenger genes. The toxin gene, for example, can be inserted into the BamHI site of pEND4K, propagated in *E. coli*, and transformed into appropriate plant cells.

15 Example 7 - Cloning of Novel *B. thuringiensis* Genes Into Baculoviruses

The novel genes of the invention can be cloned into baculoviruses such as *Autographa californica* nuclear polyhedrosis virus (AcNPV). Plasmids can be constructed that contain the AcNPV genome cloned into a commercial cloning vector such as pUC8. The AcNPV genome is modified so that the coding region of the polyhedrin gene is removed and a unique cloning site for a passenger gene is placed directly behind the polyhedrin promoter. Examples of such vectors are pGPB6874, described by Pennock et al. (Pennock, G.D., Shoemaker, C. and Miller, L.K. [1984] Mol. Cell. Biol. 4:399-406), and pAC380, described by Smith et al. (Smith, G.E., Summers, M.D. and Fraser, M.J. [1983] Mol Cell. Biol. 3:2156-2165). The gene coding for the novel protein toxin of the invention can be modified with BamHI linkers at appropriate regions both upstream and downstream from the coding region and inserted into the passenger site of one of the AcNPV vectors. Other baculoviruses can be used, e.g., *Spodoptera exigua* nuclear polyhedrosis virus (SeNPV) and *Heliothis zea* nuclear polyhedrosis virus (HzNPV). Each of these viruses is specific for its own host with little activity for other insects (i.e., SeNPV will infect *Spodoptera exigua* but not *Heliothis zea*, and vice versa).

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Example 8 - Propagation of Viruses

The viruses are propagated by infecting the appropriate larvae. This can be accomplished by direct application of inoculum to the surface of diet cups and placing fourth instar larvae on the diet as described by Maruniak (Maruniak, J.E. [1986] The Biology of Baculoviruses, Vol. 1, pp. 129-175, R.R. Granados and B.A. Federici, eds., CRC Press). Larvae are then harvested at six days post infection and NPV isolated as follows. The larvae are collected, homogenized and filtered through cheesecloth. The filtrate is then centrifuged for 15 minutes at 8,000 xg. The resulting pellet is resuspended in buffer that contains 0.01 M Tris-HCl pH 7.8 and 1.0 mM EDTA, (TE buffer). The suspension is layered onto a 20-90% sucrose gradient and centrifuged for 60 min at 100,000 xg. The polyhedra, localized as a defined band at approximately 60%, is removed and diluted in TE buffer. The polyhedra are then isolated by centrifugation for 30 min at 10,000 xg.

The purified polyhedral pellet is resuspended in TE buffer and alkali extracted with an equal volume of 0.2 M Na₂CO₃ pH 10.9, 0.17 M NaCl, and 1.0 mM EDTA. The extraction is allowed to proceed for 60 min at room temperature with continuous mixing. The larval occluded virus alkali liberated or LOVAL are isolated by centrifugation and a 20-90% sucrose at 100,000 xg for 60 min. These represent single, double or multiply embedded virions. All bands are recovered, diluted into TE buffer and centrifuged at 100,000 xg for 60 min. The resulting pellet is resuspended in TE buffer containing 1.0 mM PMSF.

The polypeptide components of the SeNPV and HzNPV LOVAL fractions are analyzed by polyacrylamide gel electrophoresis (PAGE) in the presence of sodium dodecyl sulfate (SDS) by the method of Laemmli (Laemmli, U.K., [1970] Nature [London] 227:680-685). The molecular weights determined from the relative electrophoretic mobilities are shown in Table 5. Following the above procedures, we identified thirteen and fourteen polypeptides for the HzNPV and SeNPV LOVAL preparations, respectively.

A bioassay of these preparations demonstrated minimal infectivity of the SeNPV LOVAL in *Heliothis zea* larvae. The converse was also found to be true; the infectivity of HzNPV LOVAL in *Spodoptera exigua* was limited.

Example 9 - Construction of Hybrid Virus

Virulence/specificity of baculoviruses is conferred by fusogen components in the virion envelope. Using known techniques for alteration of the target recognition of Epstein-Barr virus with re-associated Sendai virus envelopes (Shapiro, I.M. et al. [1982] Science 219:1225-1228; Volsky, D.J. et al. [1980] Proc. Natl. Acad. Sci. U.S.A. 77:5453-5457; Volsky, D.J. et al. [1979] Proc. Natl. Acad. Sci. U.S.A. 76:5440-5444) we constructed a hybrid virus by re-associating solubilized envelope proteins from SeNPV LOVAL with HznPV. The procedure involved suspending the LOVAL fraction in 40 mM Tris-acetate pH 8.0 containing 1.0 mM EDTA (TAE buffer). This suspension was incubated with octyl glucoside 1:2 (w/w) at 37°C for 4 hr with continuous shaking. Insoluble proteins were removed by centrifugation for 80 min at 100,000 xg. The supernatant containing the solubilized viral proteins was combined with purified HznPV LOVAL 1:1 (w/w). The detergent was removed by dialysis at 4°C for 24 hr with 3 changes of TAE buffer. The hybrid virus was isolated by centrifugation for 60 min at 100,000 xg through a 10% sucrose cushion.

The resultant hybrid virus was then used to infect both *Spodoptera exigua* and *Heliothis zea* larvae. The results of this study are reported in Table 6. These data show that the hybrid HznPV has activity against *Spodoptera exigua* that HznPV does not.

To determine which polypeptide(s) were responsible for conferring virulence, the octyl glucoside extract of SeNPV LOVAL was radiolabeled with ¹²⁵I and combined with unlabeled HznPV LOVAL. An autoradiogram of the SDS-PAGE of the octyl glucoside extract SeNPV showed three polypeptides present in the soluble fraction. Similar analysis of the hybrid virus showed all three SeNPV proteins to be associated with the HznPV hybrid. The relative molecular weights of these polypeptides as determined by electrophoretic mobility are shown in Table 7.

We have demonstrated an alteration of NPV host range following construction of a hybrid virus. We conclude that one of the proteins contained in the octyl glucoside extract confers virulence for *Spodoptera exigua* to HznPV. Thus, we have demonstrated that it is possible to confer virulence from one occluded NPV to another through re-association of envelope proteins.

Example 10 - Construction of a Hybrid Toxin Using NPV Fusogenic Protein to Replace *Bacillus thuringiensis* Recognition Protein

Construction of the hybrid virus demonstrates that the proteins in the envelope of the NPV are responsible for altering the virulence. We have identified the three putative proteins involved with this recognition and purified them for determination of individual contribution to the recognition event necessary for the observed alteration in virulence. This determination can be accomplished by constructing three different hybrid viruses with the three individual purified proteins isolated from octylglucoside fraction and HznPV, as previously described. These are bioassayed individually to determine which hybrid virus confers virulence. The protein responsible for recognition so identified can be purified and the amino acid sequence determined from reverse phase HPLC purified tryptic fragments of the protein. The amino acid sequence can be used to construct oligonucleotide probes which can be used to identify and isolate the gene that codes for the recognition fusogen from a gene library that is made to the viral DNA by standard molecular genetic techniques. The identified and isolated DNA then can be sequenced to define the open reading frame that codes for the protein. The DNA coding for the recognition fusogen can be cloned into the hybrid toxin construct in place of the *B. thuringiensis* recognition sequence using techniques described frequently.

It is well known in the art that the amino acid sequence of a protein is determined by the nucleotide sequence of the DNA. Because of the redundancy of the genetic code, i.e., more than one coding nucleotide triplet (codon) can be used for most of the amino acids used to make proteins, different nucleotide sequences can code for a particular amino acid. Thus, the genetic code can be depicted as follows:

Phenylalanine (Phe)	TTK	Histidine (His)	CAK
Leucine (Leu)	XTY	Glutamine (Gln)	CAJ
Isoleucine (Ile)	ATM	Asparagine (Asn)	AAK
Methionine (Met)	ATG	Lysine (Lys)	AAJ
Valine (Val)	GTL	Aspartic acid (Asp)	GAK
Serine (Ser)	QRS	Glutamic acid (Glu)	GAJ
Proline (Pro)	CCL	Cysteine (Cys)	TGK
Threonine (Thr)	ACL	Tryptophan (Trp)	TGG
Alanine (Ala)	GCL	Arginine (Arg)	WGZ
Tyrosine (Tyr)	TAK	Glycine (Gly)	GGL
Termination signal	TAJ		

Key: Each 3-letter deoxynucleotide triplet corresponds to a trinucleotide of mRNA, having a 5'-end on the left and a 3'-end on the right. All DNA sequences given herein are those of the strand whose sequence correspond to the mRNA sequence, with thymine substituted for uracil. The letters stand for the purine or pyrimidine bases forming the deoxynucleotide sequence.

A = adenine

G = guanine

C = cytosine

T = thymine

X = T or C if Y is A or G

X = C if Y is C or T

Y = A, G, C or T if X is C

Y = A or G if X is T

W = C or A if Z is A or G

W = C if Z is C or T

Z = A, G, C or T if W is C

Z = A or G if W is A

QR = TC if S is A, G, C or T; alternatively

QR = AG if S is T or C

J = A or G

K = T or C

L = A, T, C or G

M = A, C or T

The above shows that the novel amino acid sequence of the B.t. toxin can be prepared by equivalent nucleotide sequences encoding the same amino acid sequence of the protein. Accordingly, the subject invention includes such equivalent nucleotide sequences. In addition it has been shown that proteins of identified structure and function may be constructed by changing the amino acid sequence if such changes do not alter the protein secondary structure (Kaiser, E.T. and Kezdy, F.J. [1984] Science 223:249-255). Thus, the subject invention includes mutants of the amino acid sequence depicted herein which do not alter the protein secondary structure, or if the structure is altered, the biological activity is retained to some degree.

Materials and Methods Used In the Biochemical Analysis of Hybrid Toxins

Materials

The CF-1 cell line, derived from *Choristoneura fumiferana*, was obtained from the Canadian Forestry Research Laboratories (Dr. S. Sohi, Sault Ste. Marie, Ont., Canada). Nicked diphtheria toxin was purchased from Calbiochem (San Diego, CA), and radioisotopes (^{14}C -leucine and ^{14}C -NAD) from DuPont/NEN (Boston, MA) at specific activities of 308 and 600 mCi/mmol, respectively. HD-73 *Bacillus thuringiensis* toxin crystals were isolated by NaBr gradient centrifugation. All other chemicals and reagents were of the highest commercially available purity.

Methods

5 Cell Culture

CF-1 cell culture stocks were maintained at 28° C in 75 cm² T-flasks with Grace's Insect medium (GIBCO, Compton, CA) supplemented with 10% fetal bovine serum, 2 mM L-Glutamine and 2.7 gm/l tryptose broth powder (DIFCO, Detroit, MI). Cultures were passaged daily by 1:1 splits.

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Radioiodination

The 64 kd toxic component of HD-73 was produced by digestion of HD-73 crystals (1 mg/ml) dissolved in 50 mM CAPS buffer (pH 11) with trypsin (0.1 mg/ml). Digestions were conducted at 37° C on a shaker bath for 3 hr, followed by dialysis against a 20 mM glycine-Tris buffer (pH 8.5). Radioiodinations were conducted in a reaction mix comprised of 100 µg toxin, 50 µg chloramine-T, 1 mCi of Na¹²⁵I and sufficient volume of 100 mM NaPi buffer, pH 7.0 to give a 1.0 ml final volume. The mixture was reacted at 4° C for 5 minutes, then subjected to centrifugal filtration (Centricon, by Amicon; Danvers, MA) to remove unbound ¹²⁵I.

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Cyanogen Bromide Digestions

To 7 mg of HD-73 64 kd toxin was added 8 ml of 88% formic acid and 212 mg of CNBr. The mixture was reacted for 24 hr at 25° C in the dark, then dialyzed against five 2-1 changes of 20 mM glycine-Tris buffer, pH 8.6.

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Binding Assays

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CF-1 cells were harvested by centrifugation and resuspended at a concentration of 2.94×10^5 /ml in Tyrode's solution (In gm/l: NaCl, 7.0; CaCl₂·2H₂O, 0.2; NaH₂PO₄, 0.2; KCl, 0.2; MgCl₂·6H₂O, 0.1; HEPES, 4.8; glucose, 8.0; pH 6.3) containing 1 mg/ml bovine serum albumin. For binding assays, 450 µl of cell suspension was incubated with 50 µl of unlabeled toxin or CNBr digest at various concentrations for 20 min at 25° C, then with 25 µl of iodinated toxin for an additional 20 min. The cells were then recovered and washed (3 x 5 ml of 50 mM CAPS buffer, pH 11) by vacuum filtration on Whatman GF/A filter discs, and cell-bound radioactivity was quantitated by liquid scintillation. Control binding was determined as described above but in the absence of competing ligand. Background binding to the filter discs was determined from incubations performed in the absence of cells.

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EF-2 Ribosylation Assays

Elongation factor 2 (EF-2) was extracted from raw wheat germ and partially purified as previously described (Legocki, A.B. [1979] Methods Enzymol. 50:703-712). ¹⁴C-NAD was diluted to a specific activity of 240 mCi/mmol with deionized water. Ribosylation assays were performed in a final volume of 200 µl containing 170 µl of EF-2 (0.8 mg), 20 µl of hybrid toxin or diphtheria toxin (control) and 10 µl of ¹⁴C-NAD. Toxin and EF-2 were incubated at 37° C for 20 minutes, followed by the addition of ¹⁴C-NAD and subsequent incubation for 30 minutes at 37° C. The reaction was stopped by the addition of 3 ml of ice-cold 5% trichloroacetic acid (TCA), and the precipitated protein was collected by vacuum filtration on GF/A filter discs, which were counted by liquid scintillation.

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¹⁴C-Leucine Incorporation into Protein in CF-1 Cells

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Incubations were typically conducted in a volume of 500 µl containing 450 µl of CF-1 cells suspended in cell medium at a concentration of 5×10^5 /ml and 50 µl of hybrid toxin, diphtheria toxin, HD-73 or appropriate buffer control. At varying intervals, 100 µl aliquots were withdrawn and incubated with 10 µl of

¹⁴C-leucine for 30 min. Cells were pelleted by centrifugation, discarding the supernatant. The cell pellet was solubilized by the addition of 200 µl of 0.1 N KOH, and protein was precipitated by the addition of 200 µl of ice-cold 20% TCA. After 15 min on ice, the TCA precipitate was collected by vacuum filtration on Whatman GF/B discs (Whatman Laboratory Products, Clifton, NJ) and washed twice with 3 ml of cold 10% TCA. Filter discs were counted for radioactivity as described elsewhere.

Autoradiograms developed from SDS-PAGE gels of radioiodinated HD-73 demonstrated labeling of the 64 kd active toxin protein produced by trypsin digestion. The specific activity of labeling was estimated to be 3×10^{16} cpm/mol. Figure 2 shows that unlabeled HD-73 competes with the labeled toxin for binding to CF-1 cells with an IC_{50} of 35 µg/ml. In addition, binding of radiolabeled toxin equilibrated rapidly (< 5 min), and was not reversed by wash out procedures. Saturation studies gave an estimate of $> 1 \times 10^5$ binding sites per cell. These findings demonstrate specific binding of the radiolabeled 64 kd tryptic peptide of HD-73 to CF-1 insect cells in culture. The 64 kd component is therefore considered a viable candidate for the binding site recognition portion of a hybrid toxin construct.

In order to further delineate the binding site recognition domain of the 64 kd toxin, CNBr digestions were performed to generate smaller peptides for analysis. Following dialysis through a 14 kd cutoff membrane, we obtained peptides of 18 and 19 kd molecular weights as evidenced by SDS-PAGE. Binding experiments with CF-1 cells demonstrated that this peptide mixture partially competes for iodinated 64 kd binding (Figure 3). It is therefore likely that the binding domain of HD-73 can be mapped to at least one of these two CNBr-generated peptides.

Figure 4 gives the concentration dependence for diphtheria toxin - stimulated ADP - ribosylation of wheat germ EF-2. Half maximal ribosylation was obtained at a diphtheria toxin concentration of 0.8 ng/ml. The extent of ADP-ribosylation at saturating diphtheria toxin concentrations was quite reproducible in our hands, and was therefore used as an index for quantitating hybrid toxin-catalyzed ribosylation. Figure 5 gives the results for such determinations, showing that quarter- and half-length hybrid toxins are roughly equivalent with respect to their ribosylation capacities, though 5000-fold less potent than diphtheria toxin. However, uncertainty in the relative purity of the hybrid toxin preparation makes the latter comparison approximate, and almost certainly represents a low end estimate of potency.

Figure 6 demonstrates the inhibiting effect of HD-73 toxin on the incorporation of radiolabeled leucine into protein in CF-1 cells. Half-maximal inhibition was obtained at an HD-73 concentration of 40 µg/ml, in good agreement with the binding data presented above. Additional concurrence between HD-73 binding and inhibition of protein synthesis was established for the time-course and irreversibility of the inhibitory effect.

Incubation of CF-1 cells with quarter- and half-length hybrid toxins results in a slowly developing inhibition of protein synthesis (Figure 7). From the 24-hour exposure data, we estimate a 50-fold increase in potency for the quarter-length and a 100-fold increase for the half-length hybrid toxin over that established for HD-73. The lengthened time-course and increased potency observed for the hybrid toxins indicate a mechanism of action distinct from that of HD-73. Furthermore, diphtheria toxin does not inhibit protein synthesis in CF-1 cells at concentrations up to 200 µg/ml. It is therefore unlikely that the inhibition produced by the hybrid toxin preparations is related to either the diphtheria or B.t. toxin domains by themselves, as might be the case if these two portions of the hybrid construct dissociated under experimental conditions. Rather, we conclude that these findings demonstrate an inhibitory mechanism unique to the intact hybrid toxins.

The various methods employed in the preparation of the plasmids and transformation of host organisms are well known in the art. These procedures are all described in Maniatis, T., Fritsch, E.F., and Sambrook, J. (1982) Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory, New York. Thus, it is within the skill of those in the genetic engineering art to extract DNA from microbial cells, perform restriction enzyme digestions, electrophorese DNA fragments, tail and anneal plasmid and insert DNA, ligate DNA, transform cells, prepare plasmid DNA, electrophorese proteins, and sequence DNA.

The restriction enzymes disclosed herein can be purchased from Bethesda Research Laboratories, Gaithersburg, Maryland, USA, or New England Biolabs, Beverly, Massachusetts, USA. The enzymes are used according to the invention provided by the supplier.

A subculture of an *E. coli* host containing plasmid p26, also known as pMYC26, has been deposited in the permanent collection of the Northern Research Laboratory, U.S. Department of Agriculture, Peoria, Illinois, USA. *E. coli* HB101 (pMYC26) was deposited on 18.05.88 and has the accession number NRRL B-18367. It was previously on deposit in the Mycogen Corporation Culture Collection at San Diego, California, USA. The plasmid can be obtained from the host by use of standard procedures, for example, using cleared lysate-isopycnic density gradient procedures.

Claims

1. A hybrid pesticidal protein toxin comprising a cytotoxic agent and a pest gut epithelial cell recognition portion of a protein.
- 5 2. A toxin according to claim 1, wherein the cytotoxic agent is a ribosome-inactivating enzyme obtainable from a seed of barley, rye, corn or wild bean.
3. A toxin according to claim 1, wherein the cytotoxic agent is a ribosome-inactivating enzyme selected from ricin, dianthin, saporin, gelonin, tritin, abrin and modeccin.
4. A toxin according to claim 1, wherein the cytotoxic agent is an ADP-ribosylating enzyme.
- 10 5. A toxin according to claim 2, wherein the enzyme is diphtheria toxin.
6. A toxin according to claim 5, wherein the toxin comprises the A fragment of the diphtheria toxin, plus the B fragment of the diphtheria toxin which has been truncated at the carboxyl terminus to remove the eukaryotic recognition region.
7. A toxin according to any preceding claim, which is a Bacillus thuringiensis protein toxin.
- 15 8. A toxin according to claim 7 which is expressed by a gene fragment from Bacillus thuringiensis var. kurstaki HD-73.
9. A toxin according to any preceding claim, wherein the cytotoxic agent and the protein portion are linked by a peptide linker whose length and amino-acid composition are such as to minimise susceptibility to insect protease cleavage.
- 20 10. A toxin according to claim 9, wherein the peptide linker comprises no more than four amino-acids.
11. A toxin according to claim 9 or claim 10, wherein the peptide linker contains no lysine residue.
12. DNA encoding a half-length hybrid B.t. toxin having the following amino-acid sequence:

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25      1  M S R K L F A S I L I G A L L G I G A P P S A H A G A D D V
      31  V D S S K S F V M E N F S S Y H G T K P G Y V D S I Q K G I
      61  Q K P K S G T Q G N Y D D D W K G F Y S T D N K Y D A A G Y
      91  S V D N E N P L S G K A G G V V K V T Y P G L T K V L A L K
     121  V D N A E T I K K E L G L S L T E P L M E Q V G T E E F I K
     151  R F G D G A S R V V L S L P F A E G S S S V E Y I N N W E Q
     181  A K A L S V E L E I N F E T R G K R G Q D A M Y E Y M A Q A
     211  C A G N R V R R S V G S S L S C I N L D W D V I R D K T K T
     241  K I E S L K E H G P I K N K M S E S P N K T V S E E K A K Q
     271  Y L E E F H Q T A L E H P E L S E L K T V T G T N P V F A G
     301  A N Y A A W A V N V A Q V I D S E T A D N L E K T T A A L S
     331  I L P G I G S V M G I A D G A V H H N T E E I V A Q S I A L
     361  S S L M V A Q A I P L V G E L V D I G F A A Y N F V E S I I
     391  N L F Q V V H N S Y N R P A Y S P G H K T Q P P L H D G Y A
     421  V S W N T V E D S I I R T G F Q G E S G H D I K I T A E N T
     451  P L P I A G V L L P T I P G K L D V N K S K T H I S V N G R
     481  K I R M R C R A I D G D V T F C R P K S P V Y V G N G V H A
     511  N L F R T V S Q L T R E I Y T N P V L E N F D G S F R G S A
     541  Q G I E R S I R S P H L M D I L N S I T I Y T D A H R G Y Y
     571  Y W S G H Q I M A S P V G F S G P E F T F P L Y G T M G N A
     601  A P Q Q R I V A Q L G Q G V Y R T L S S T L Y R R P F N I G
     631  I N N Q Q L S V L D G T E F A Y G T S S N L P S A V Y R K S
     661  G T V D S L D E I P P Q N N N V P P R Q G F S H R L S H V S
     691  M F R S G F S N S S V S I I R A P M F S W I H R S A E F N N
     721  I I A S D S I T Q I P A V K G N F L F N G S V I S G P G F T
     751  G G D L V R L N S S G N N I Q N R G Y I E V P I H F P S T S
     781  T R Y R V R V R Y A S V T P I H L N V N W G N S S I F S N T
     811  V P A T A T S L D N L Q S S D F G Y F E S A N A P T S S L G
     841  N I V G V R N F S G T A G V I I D R F E F I P V T A T L E
     871

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13. DNA encoding a quarter-length hybrid B.t. toxin having the following amino-acid sequence:

1 MSRKLFASILIGALLGIGAPPSPAHAAGADDV
 31 VDS SKS FV MEN FSS YHG TKPGYVDSIQKGI
 61 QKPKSGTQGN YDD DWKGFYSTDNKYDAAGY
 5 91 SVDNENPLSGKAGGVVKVTPGLTKVLAALK
 121 VDN AETIKKELGLSLTEPLMEQVGT EEFIK
 151 RFGD GASRVVLSLPFAEGSSSV EYINNWEQ
 181 AKALSVELEINFETRGRGQDAMY EYMAQA
 211 CAGNRVRRSVGS SLSCLNLDWDVIRDKTKT
 10 241 KIESLKEHGP IKNKMS ESEPNKT VSE EKAKQ
 271 YLEEFHQTALEHPELSELKT VGTNPVPAG
 301 ANYAAWAVNV AQVIDSE TADNLEKTTAALS
 331 ILPGIGSVMG IADGAVHHNTE EIVAQSIAL
 361 SSLMVAQAIP LVGELVDIGFAAYNFVESII
 391 NLFQVVHNSYN RPAYSPGHKTQ PFLHDGYA
 15 421 VSWNTVEDS IIR TGFGGESGHD IKITAE NT
 451 PLPIAGVLLPT IPGKLDV NKSKTHISVNGR
 481 KIRMRCRAIDG DVTFCRPKSPVYV GNGVHA
 511 GAAPMF SWIHRS AEFNNIIASDSITQIPAV
 541 KGNFLFNGSV VISGPGFTGGDLVRLNSSGNN
 20 571 IQNRGVIEVPI HFPSTSTRYRV RYASVT
 601 PIHLNVNWGNS SIFSNTPATATSLDNLQS
 631 SDFGYFESANA FTSSLGNI VGV RNFSGTAG
 661 V I I D R F E F I P V T A T L E
 691

25 14. DNA according to claim 12, having the following nucleotide sequence:

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10 20 30 40 50 60 70 80
 GTGAGCAGAAAACTGTTTGGCTCAATCTTAATAGGGGCGCTACTGGGGATAGGGGCCCCACCTTCAGCCCCATGCAGGGGC
 5 90 100 110 120 130 140 150 160
 TGATGATGTTGTTGATTCTTCTAAATCTTTGTGATGGAACCTTTCTTCGTACCCACGGCACTAAACCTGGTTATGTAG
 170 180 190 200 210 220 230 240
 ATTCCATTCAAAAAGGTATACAAAAGCCAAAATCTGGTACACAAGGAAATTATGACGATGATTGGAAAGGGTTTTATAGT
 10 250 260 270 280 290 300 310 320
 ACCGACAATAAATACGACGCTGCGGGATACTCTGTAGATAATGAAAAACCGCTCTCTGGAAAAGCTGGAGGCGTGGTGAA
 330 340 350 360 370 380 390 400
 AGTGACGTATCCAGGACTGACGAAGGTTCTCGCACTAAAAGTGGATAATGCCGAACTATTAAGAAAGAGTTAGGTTAA
 410 420 430 440 450 460 470 480
 GTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTTATCAAAAGGTTCCGGTGATGGTGCTTCGCGTGTAGTG
 15 490 500 510 520 530 540 550 560
 CTCAGCCTTCCCTTCGCTGAGGGGAGTTCTAGCGTTGAATATATTAATAACTGGGAACAGGCGAAAGCGTTAAGCGTAGA
 570 580 590 600 610 620 630 640
 ACTTGAGATTAATTTTGAACCGTGGAAAACGTGGCCAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAA
 20 650 660 670 680 690 700 710 720
 ATCGTGTACGGCGATCAGTAGGTAGCTCATTGTCTATGCATAAATCTTGATTGGGATGTCATAAGGGATAAACTAAGACA
 730 740 750 760 770 780 790 800
 AAGATAGAGTCTTTGAAAGAGCATGGCCCTATCAAAAATAAATGAGCGAAAGTCCCAATAAAACAGTATCTGAGSAAAA
 810 820 830 840 850 860 870 880
 25 AGCTAAACATACCTAGAGAATTTTCATCAACCGGCATTAGAGCATCCTGAATTGTCAGAACTTAAACCGTTACTGGGA
 890 900 910 920 930 940 950 960
 CCAATCCTGTATTTCGCTGGGGCTAACTATGCGGCGTGGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGAT
 970 980 990 1000 1010 1020 1030 1040
 30 AATTTGGAAAAGACAACCTGCTCTTTTCGATACTTCCTGGTATCGGTAGCGTAATGGGCATTGCAGACGGTCCCGTTCA
 1050 1060 1070 1080 1090 1100 1110 1120
 CCACAATACAGAAGAGATAGTGGCACAATCAATAGCTTTATCGTCTTTAATGGTTGCTCAAGCTATTCCATTGGTAGGAG
 1130 1140 1150 1160 1170 1180 1190 1200
 35 AGCTAGTTGATATTGGTTTCGCTGCATATAATTTTGTAGAGAGTATTATCAATTTATTTCAGTAGTTCATAATTCGTAT
 1210 1220 1230 1240 1250 1260 1270 1280
 AATCGTCCCGCTATTCTCCGGGGCATAAAACGCAACCATTTCTTCATGACGGGTATGCTGTCAAGTTGGAACACTGTTGA
 1290 1300 1310 1320 1330 1340 1350 1360
 40 AGATTGCGATAATCCGAACCTGGTTTCAAGGGGAGAGTGGGCACGACATAAAAAATTACTGCTGAAAAATACCCCGCTTCCAA
 1370 1380 1390 1400 1410 1420 1430 1440
 TCGCGGGTGTCTTACTACCGACTATTCTCGGAAAGCTGGACGTTAATAAGTCCAAGACTCATATTTCCGTAAATGGTCGG
 1450 1460 1470 1480 1490 1500 1510 1520
 45 AAAATAAGGATGCGTTGCAGAGCTATAGACGGTGATGTAACCTTTTGTGCGCCCTAAATCTCCTGTTTATGTTGGTAATGG
 50
 55

1530 1540 1550 1560 1570 1580 1590 1600
 TGTGCTGCTAACCTGTTTCGAACAGTTTCCCAATTAAACAGAGAGAAATTATACAAACCCAGTATTAGAAAAATTTTGATG
 1610 1620 1630 1640 1650 1660 1670 1680
 GTAGTTTTCGAGGCTCGGCTCAGGGCATAGAAAGAGTATTAGGAGTCCACATTTGATGGATATACTTAACAGTATAACC
 1690 1700 1710 1720 1730 1740 1750 1760
 ATCTATACGGATGCTCATAGGGGTATTATTATTGGTCAGGGCATCAAATAATGGCTTCTCCTGTAGGGTTTTTCGGGGCC
 1770 1780 1790 1800 1810 1820 1830 1840
 AGAATTCACCTTTCCGCTATATGCAACTATGGGAAATGCAGCTCCACAACACGTATGTGTGCTCAACTAGGTCAGGGCG
 1850 1860 1870 1880 1890 1900 1910 1920
 TGTATAGAACATTATCGTCCACTTTATATAGAAGACCTTTTAATATAGGGATAAATAATCAACAACATCTCTCTTGAC
 1930 1940 1950 1960 1970 1980 1990 2000
 GGGACAGAATTTGCTTATGGAACCTCCTCAAATTTGCCATCCGCTGTATACAGAAAAGCGGAACGGTAGATTCGCTGGA
 2010 2020 2030 2040 2050 2060 2070 2080
 TGAATACCGCCACAGAATAACAACGTGCCACCTAGGCAAGGATTTAGTCATCGATTAAGCCATGTTTCAATGTTTCGTT
 2090 2100 2110 2120 2130 2140 2150 2160
 CAGGCTTTAGTAATAGTAGTGAAGTATAATAAGAGCTCCTATGTTCTCTTGATACATCGTAGTGCTGAATTTAATAAT
 2170 2180 2190 2200 2210 2220 2230 2240
 ATAATTCATCGGATAGTATTACTCAATCCCTGCAGTGAAGGAAACCTTTCTTTTAATGGTTCTGTAAATTCAGGACC
 2250 2260 2270 2280 2290 2300 2310 2320
 AGGATTTACTGGTGGGGACTTAGTTAGATTAAATAGTAGTCGAAATAACATTGAGATAGAGGGTATATTGAAGTTCCAA
 2330 2340 2350 2360 2370 2380 2390 2400
 TTCACCTCCCATCGACATCTACCAGATATCGAGTTCGTACGGTATGCTTCTGTAAACCCGATTACCTCAACGTTAAT
 2410 2420 2430 2440 2450 2460 2470 2480
 TGGGGTAATTCATCCATTTTTCCAATACAGTACCAGCTACAGCTACGTCAATTAGATAATCTACAATCAAGTGATTTTGG
 2490 2500 2510 2520 2530 2540 2550 2560
 TTATTTTGAAAGTCGCAATGCTTTTACATCTTCATTAGGTAAATATAGTAGGTGTTAGAAATTTTAGTGGGACTGCAGGAG
 2570 2580 2590 2600 2610 2620
 TGATAATAGACAGATTGTAATTTATCCAGTTACTGCAACACTCGAGTAGTAGGTGACAGCTT

15. DNA according to claim 13, having the following nucleotide sequence:

10 20 30 40 50 60 70 80
 GTGAGCAGAAAAGCTGTTTGGCTCAATCTTAATAGGGGCGCTACTGGGGATAGGGGCCCCACCTTCAGCCCATGCAGGGCC
 90 100 110 120 130 140 150 160
 TGATGATGTTGTTGATTCTTCTAAATCTTTTGTGATGGAAAACTTTTCTTCGTACCACGGGACTAAACCTGGTTATGTAG
 170 180 190 200 210 220 230 240
 ATTCATTCAAAAAGGTATACAAAAGCCAAAATCTGGTACACAAGGAAATTATGACGATGATTGGAAGGGTTTTATAGT
 250 260 270 280 290 300 310 320
 ACCGACAATAAATACGACGCTGCGGGATACCTCTGTAGATAATGAAAACCCGCTCTCTGGAAGAGCTGGAGGCGTGGTGAA
 330 340 350 360 370 380 390 400
 AGTGACGTATCCAGGACTGACGAAGGTTCTCGCACTAAAAGTGGATAATGCCGAACTATTAAAGAAAGAGTTAGGTTTAA
 410 420 430 440 450 460 470 480
 GTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTTATCAAAAGGTTCCGGTGATGGTGCTTCGCGTGTAGT
 490 500 510 520 530 540 550 560
 CTCAGCCTTCCCTTCGCTGAGGGGAGTTCTAGCGTTGAATATATTAATAACTGGGAACAGGCGAAAGCGTTAAGCGTAGA
 570 580 590 600 610 620 630 640
 ACTTGAGATTAATTTTGAAACCCGTGGAACCGTGGCCAAGATGCGATGTATGAGTATATGGCTCAAGCCTCTGCAGGAA

650 660 670 680 690 700 710 720
 ATCGTGTCAGGCGATCAGTAGGTAGCTCATTGTCTATGCATAAAATCTTGATTGGGATGTCATAAGGGATAAAACTAAGACA
 730 740 750 760 770 780 790 800
 5 AAGATAGAGTCTTTGAAAGAGCATGGCCCTATCAAAAATAAAATGAGCGAAAGTCCCAATAAACAGTATCTGAGGAAAA
 810 820 830 840 850 860 870 880
 AGCTAAACAATACCTAGAGAATTTTCATCAACGGCATTAGAGCATCCTGAATTGTCAGAACTTAAACCGTTACTGGGA
 890 900 910 920 930 940 950 960
 10 CCAATCCTGTATTCGCTGGGGCTAACTATGCGGCGTGGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGAT
 970 980 990 1000 1010 1020 1030 1040
 AATTGGAAAAGACAACTGCTGCTCTTCGATACCTCCTGGTATCGGTAGCGTAATGGGCATTGCAGACGGTGCCGTTCA
 1050 1060 1070 1080 1090 1100 1110 1120
 CCACAATACAGAAGAGATAGTGGCACAATCAATAGCTTTATCGTCTTTAATGGTTGCTCAAGCTATTCCATTGGTAGGAG
 1130 1140 1150 1160 1170 1180 1190 1200
 15 AGCTAGTTGATATTGGTTTCGCTGCATATAATTTGTAGAGAGTATTATCAATTTATTTCAAGTAGTTTCATAATTCTGAT
 1210 1220 1230 1240 1250 1260 1270 1280
 AATCGTCCCGCTATTCTCCGGGCGATAAAACGCAACCATTTCTTCATGACGGGTATGCTGTGTCAGTTGGAACACTGTTGA
 1290 1300 1310 1320 1330 1340 1350 1360
 20 AGATTCGATAATCCGAACTGGTTTTCAAGGGGAGAGTGGGCACGACATAAAATTAAGTCTGCTGAAAATACCCCGCTCCAA
 1370 1380 1390 1400 1410 1420 1430 1440
 TCGCGGGTGTCTACTACCGACTATTCTCGGAAAGCTGGACGTTAATAAGTCCAAGACTCATATTTCCGTAAATGGTCGG
 1450 1460 1470 1480 1490 1500 1510 1520
 25 AAAATAAGGATGCGTTGCAGAGCTATAGACGGTGTAACTTTTGTGCGCCCTAAATCTCCTGTTTATGTTGGTAATGG
 1530 1540 1550 1560 1570 1580 1590 1600
 TGTGCATGCAGGTGCAGCTCCTATGTTCTCTGGGATACATCGTAGTGCTGAATTTAATAATATAATTGCATCGGATAGTA
 1610 1620 1630 1640 1650 1660 1670 1680
 30 TTAAGTCAAATCCCTGCAGTGAAGGGAACTTTCTTTTAAATGGTTCTGTAATTTCAAGGACCAGGATTTACTGGTGGGGAC
 1690 1700 1710 1720 1730 1740 1750 1760
 TTAGTTAGATTAAATAGTAGTCGAAATAACATTGAGAAATAGAGGGTATATTGAAGTTCCAATTCACTTCCCATCGACATC
 1770 1780 1790 1800 1810 1820 1830 1840
 35 TACCAGATATCGAGTTCTGTACGGTATGCTTCTGTAACCCCGATTCACTCAACGTTAATTGGGGTAATTCATCCATTT
 1850 1860 1870 1880 1890 1900 1910 1920
 TTTCCAATACAGTACCAGCTACAGCTACGTCATTAGATAATCTACAATCAAGTGATTTTGGTTATTTTGAAGTCCGCAAT
 1930 1940 1950 1960 1970 1980 1990 2000
 40 GCTTTTACATCTTCATTAGGTAATATAGTAGGTGTTAGAAATTTAGTGGGACTGCAGGAGTGATAATAGACAGATTGGA
 2010 2020 2030 2040
 ATTTATTCCAGTTACTGCAACACTCGAGTAGGTGCGACAGCTT

16. A toxin active against lepidopteran insects, having the amino-acid sequence shown in claim 12 or
 45 claim 13, or a mutant thereof which has an unaltered protein secondary structure and/or at least part of the
 biological activity.

17. A recombinant DNA transfer vector comprising DNA having all or part of the nucleotide sequence
 which codes for the amino-acid sequence shown in claim 12 or claim 13.

18. A DNA transfer vector according to claim 17, transferred to and replicated in a prokaryotic or
 50 eukaryotic host.

19. A microorganism capable of expressing a toxin having the amino-acid sequence shown in claim 12
 or claim 13.

20. A microorganism transformed with a DNA transfer vector comprising a cytotoxic agent and a protein
 portion as defined in any of claims 1 to 11.

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21. A microorganism according to claim 19 or claim 20, which is a species of Pseudomonas, Azobacter, Erwinia, Serratia, Klebsiella, Rhizobium, Rhodopseudomonas, Methylophilus, Agrobacterium, Acetobacter or Alcaligenes; a prokaryote selected from Enterobacteriaceae, Bacillaceae, Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudomonadaceae, Azotobacteraceae and Nitrobacteraceae; or a lower eukaryote selected
5 from Phycomycetes, Ascomycetes and Basidiomycetes.

22. A microorganism according to claim 21, which is Pseudomonas, e.g. Pseudomonas fluorescens.

23. A microorganism according to claim 19 or claim 20, which is a pigmented bacterium, yeast or fungus.

24. A microorganism according to any of claims 19 to 23, which is pigmented and phylloplane-adherent.

10 25. Substantially intact cells of a unicellular microorganism according to any of claims 19 to 24, containing the toxin.

26. Cells according to claim 25, as obtained by treatment with iodine or other chemical or physical means to prolong the insecticidal activity in the environment.

27. A method for controlling insects, which comprises administering to the insects or to their
15 environment a microorganism or cells according to any of claims 19 to 26.

28. A method according to claim 27, wherein the insects belong to the order of lepidoptera, coleoptera, diptera, hemiptera, dermaptera or orthoptera.

29. A method according to claim 27, wherein the insects are arachids, gastropods or worms, e.g. nematodes or platyhelminths.

20 30. A method according to any of claims 27 to 29, wherein administration is to the rhizosphere, to the phylloplane, or to a body of water.

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Figure 1

Enzyme	No. Cuts	1	620	1239	1859	2479	3098	3718
AccI	2.			1	1			
AflIII	3.		1				1	1
AluI	10.		1	1	1	2	1	2
Asp718	1.					1		
AsuII	1.		1					
AvaI	1.				1			
AvrII	2.			1		1		
BanI	1.					1		
BanII	1.			1				
BbvI has no cut site								
BclI	2.				1		1	
BglI	1.			1				
BinI has no cut site								
BsmI	5.2				1		1	1
BspMI has no cut site								
BspMII	1.						1	
BssHII	1.					1		
CfrI has no cut site								
Cfr10I has no cut site								
ClaI	4. 1			1		1	1	
DdeI	8.	1	1	1	1	1	1	1
DpnI	6.	1			1	1	1	1
DraI	3.					1		1
DraII	1.					1		
EcoRI	2.	1		1				
EcoRI'	32.	12121	11	1	2	1	211111	3
EcoRI*	45.	12131111	223	1	2	2	112	2
EcoRV	3.		2		1			
Fnu4HI	6.		11	1		1		11
FnuDI	2.			1		1		
FnuDII	2.		1			1		
FokI has no cut site								
GdIII	1.					1		
GsuI has no cut site								
HaeII	1.						1	
HaeIII	2.			1		1		
HgaI	2.	1					1	
HgiEII has no cut site								
HhaI	5.				2	2	1	
HindIII	1.							1
HinFI	16.	1	1	1	1	2	1	2
HinPI	5.				2	2	1	
HpaII	5.	1	1					1
HphI	4.				1	1	1	1
KpnI	1.					1		
MaeI	12.	111	11	1	1	1	13	
MaeII	15.		1	1	1	11	1	1
MaeIII	12.	11			1	1	11	1
MboI	6.	1			1		1	1
MboII	15.	1	1	11	1	1	1	1
MnlI has no cut site								
NheI	1.						1	
NlaIII	8.	1		1		1	1	2
NlaIV	8.	1	1	1	1	1		1

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Figure 2

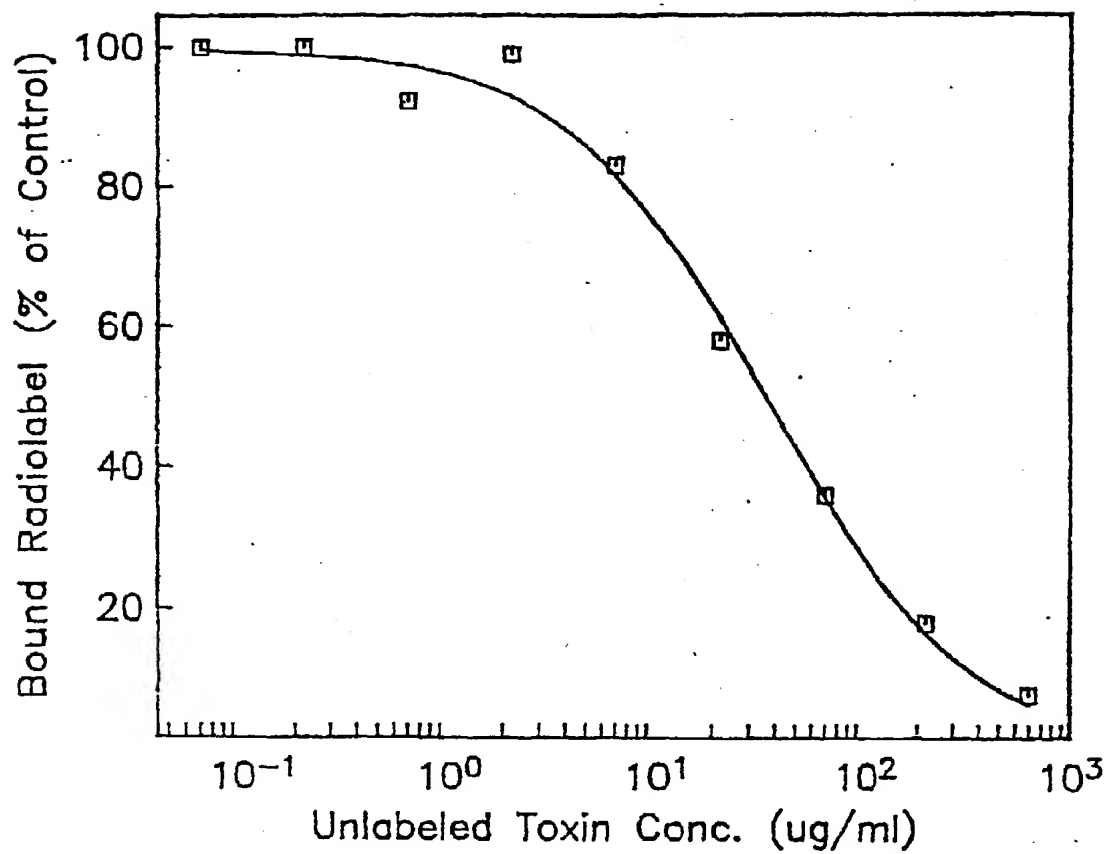


Figure 3

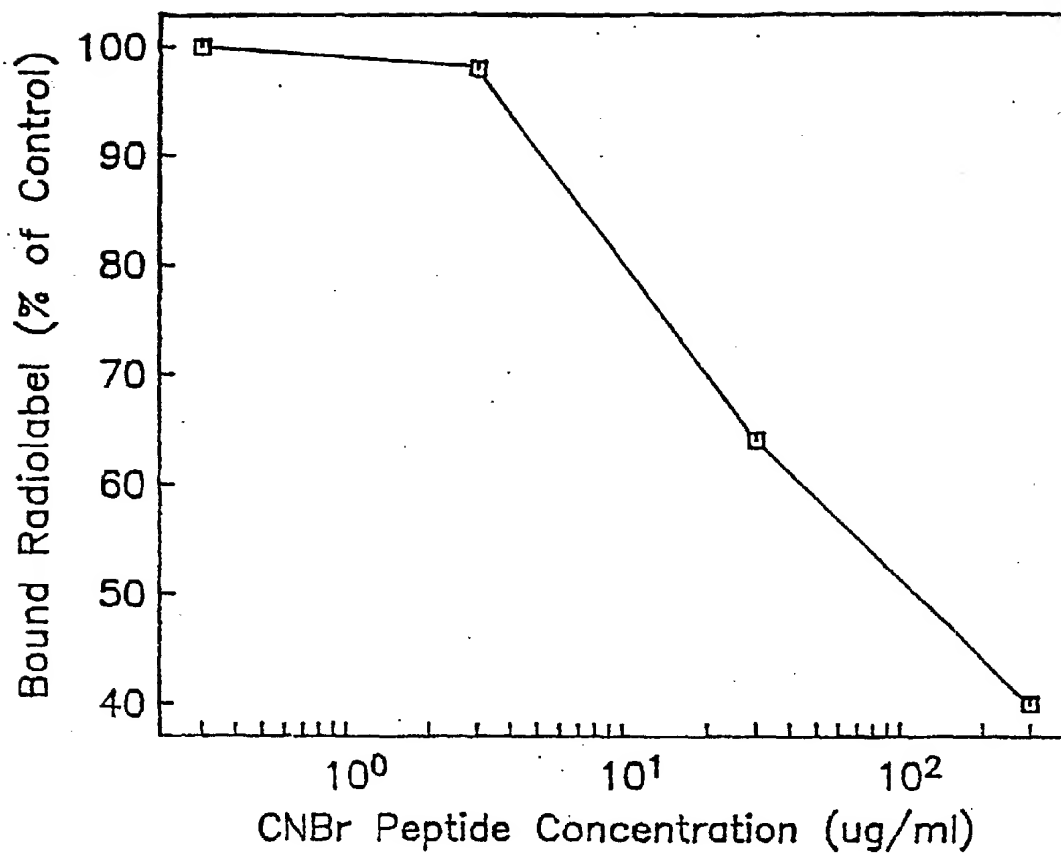


Figure 4

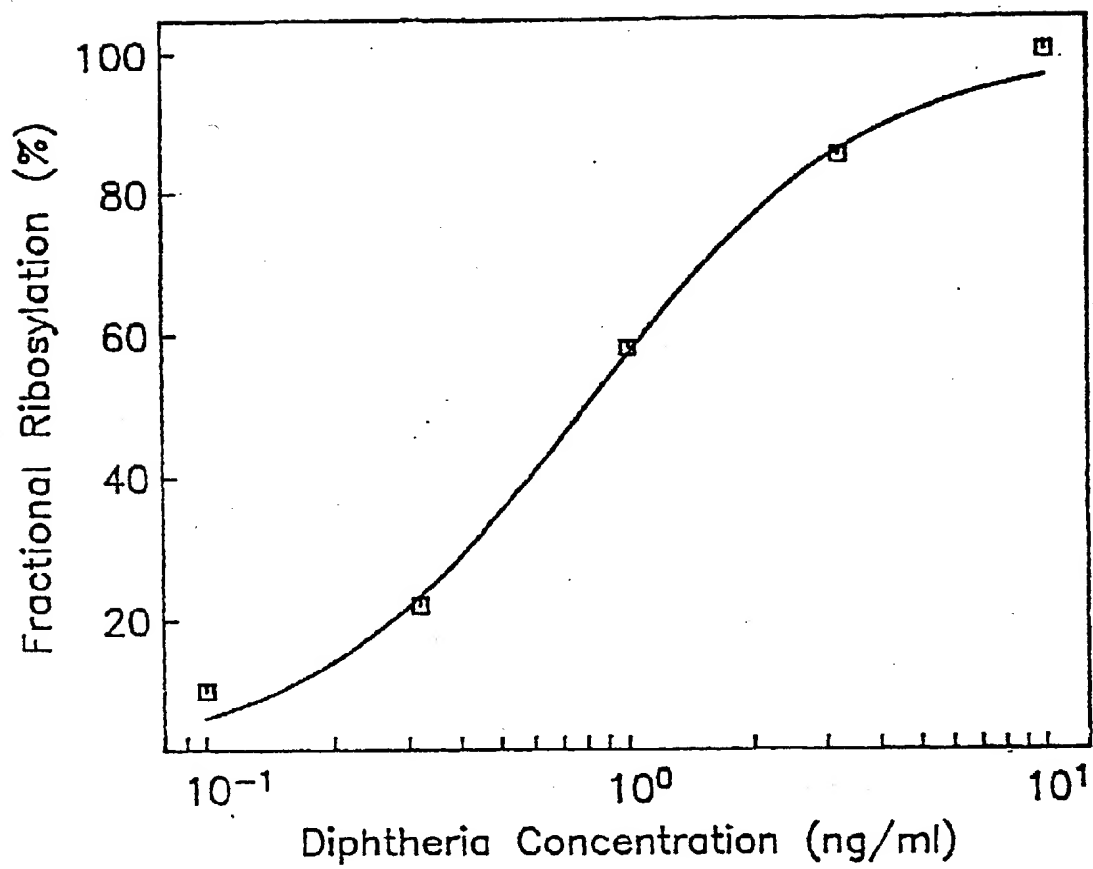


Figure 5

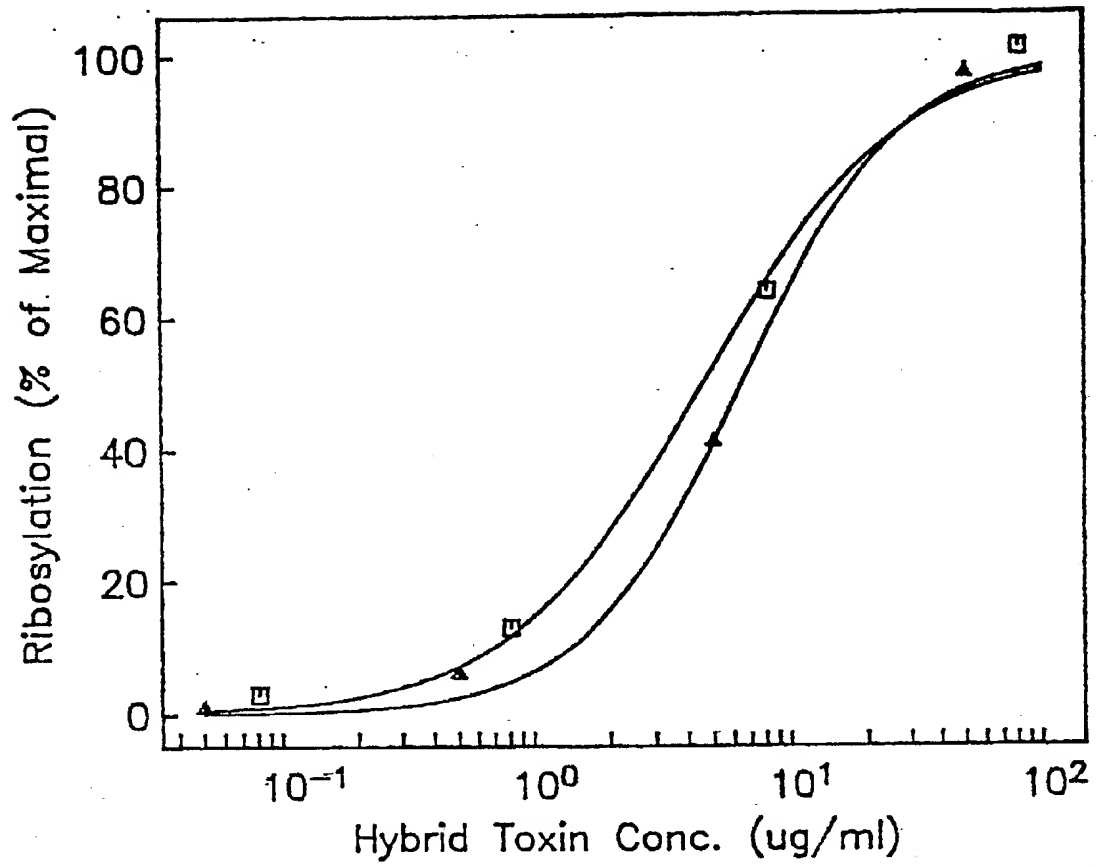


Figure 6

HD-73 Inhibition of Protein Synthesis in CF-1 Cells

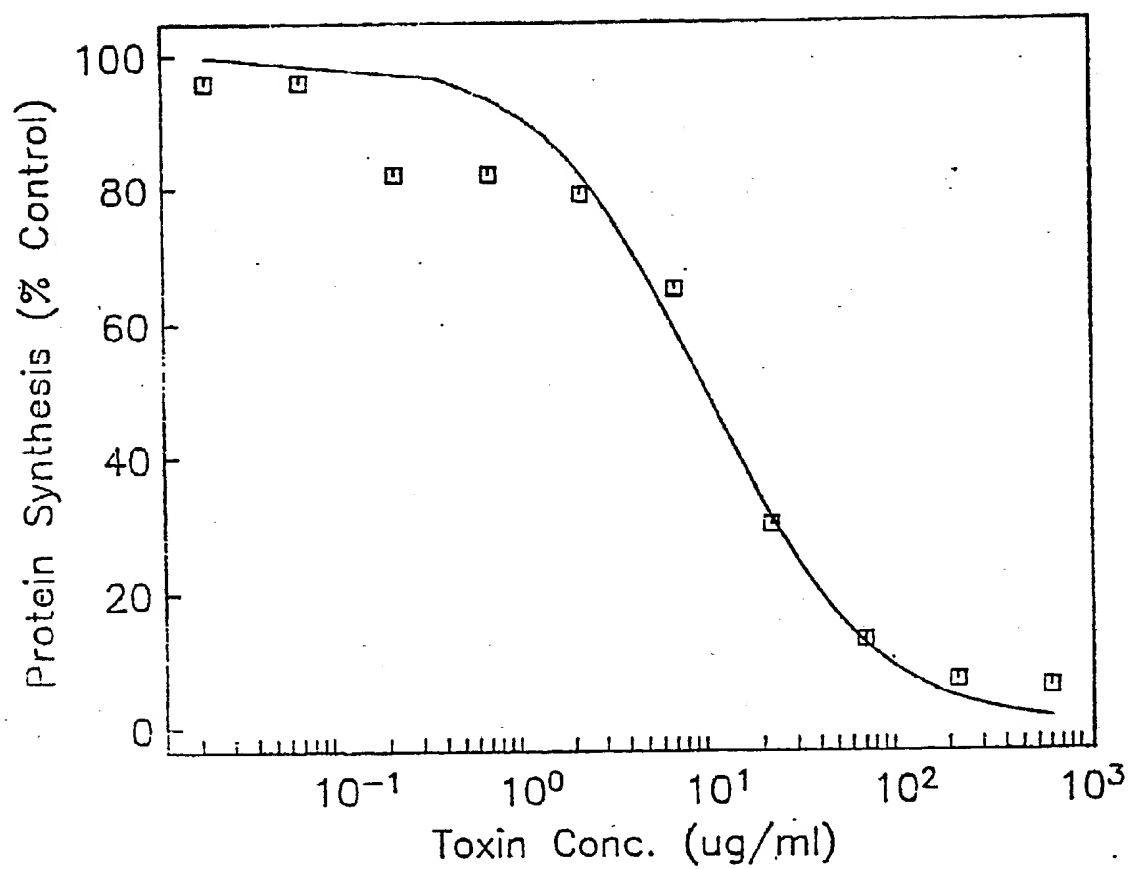


Figure 7

INHIBITION OF CF-1 CELL PROTEIN SYNTHESIS BY HYBRID TOXINS

